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**TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1764

U S APPLICATION NO (If known see 37 CFR §1.5)

09/646569

INTERNATIONAL APPLICATION NO

INTERNATIONAL FILING DATE

PCT/DE99/00909

19 MARCH 1999

PRIORITY DATE CLAIMED

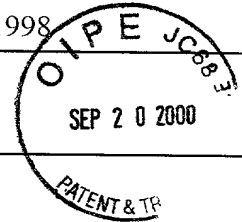
20 MARCH 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE

APPLICANT(S) FOR DO/EO/US

SPECHT, Thomas, et al.



Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371
3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1)
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date
5. ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
6. ☒ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5))

Items 11. to 16. below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included.
13. ☒ A **FIRST** preliminary amendment.
 - ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information: PAPER COPY OF SEQUENCE LISTING AND DISKETTE COPY

SCH 1764

(November 1998)

International Application No.	:	PCT/DE99/00909
International Filing Date	:	19 MARCH 1999
Priority Date(s) Claimed	:	20 MARCH 1998
Applicant(s) (DO/EO/US)	:	SPECHT, Thomas, et al.

Title: HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE

Commissioner for Patents
Washington, D.C. 20231

SIR:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

IN THE CLAIMS:

- Claim 4, line 3, after "178" insert --of Claim 3--;
- Claim 5, line 1, delete "claims 1 to 4" and insert --Claim 3--;
- Claim 6, line 1, delete "claims 1 to 4" and insert --Claim 3--;
- Claim 7, line 2, delete "claims 1 to 6" and insert --Claim 3--;
- line 4, delete "claims 1 to 6" and insert --Claim 3--;
- Claim 8, line 1, delete "claims 1 to 7" and insert --Claim 3--;
- Claim 9, line 1, delete "claims 1 to 7" and insert --Claim 3--;
- Claim 10, lines 1 and 2, delete "one of claims 1 to 9" and insert --Claim 3--;
- Claim 11, line 2, delete "one of claims 1 to 9" and insert --Claim 3--;
- Claim 13, lines 1 and 2, delete "one of claims 11 and 12" and insert --Claim 11--;
- Claim 14, lines 1 and 2, delete "claims 1 to 10" and insert --Claim 3--;
- Claim 16, line 3, delete "one of claims 1 to 10" and insert --Claim 3--;
- Claim 18, line 1, delete "one of claims 16 or 17" and insert --Claim 16--;
- Claim 19, line 2, delete "claims 16 to 18" and insert --Claim 16--;

[illegible]

Claim 36, line 1, delete "claims 1 to 7" and insert --Claim 3--.

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

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Attorney for Applicants

AJZ:jmm

Human Nucleic Acid Sequences from Normal Breast Tissue

The invention relates to human nucleic acid sequences from breast tissue, which code for gene products or parts thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death in women is breast cancer, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

It has now been found that this error possibility can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID 178, which play a role as candidate genes in breast tumors, have now been found.

Nucleic acid sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a part thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178
 - b) an allelic variation of the nucleic acid sequences named under a)
- or
- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178 or a complementary or

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allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID No. 178, which are expressed elevated in normal breast tissue or are expressed reduced in breast tumor tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, ϕ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

A control or regulatory sequence is defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the

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heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides according to the sequence protocols Seq. ID Nos. 77-85, 87, 88, 90, 91, 93, 95-108, 112-117, 119, 122, 124-126, 132, 133, 135, 137-160 and 179-209.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID Nos. 77-85, 87, 88, 90, 91, 93, 95-108, 112-117, 119, 122, 124-126, 132, 133, 135, 137-160 and 179-209 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by

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The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq.

With the nucleic acids according to the invention (cDNA sequences), genomic BAC, PAC and Cosmid libraries are screened and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and Cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and Cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and Cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID No. 179, for use as vehicles for gene transfer.

Nucleic acids= Nucleic acids in this invention are defined as:

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence.

Singleton = A contig that contains only one sequence.

N = selectively the nucleotide A, T, G or C.

Explanation of the alignment parameters

maximum pads per read = maximum number of insertions

Explanation of Figures

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

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The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for tumor-related candidate genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

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Figures 2b1-2b4 illustrate the lengthening of the breast tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another).

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

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Algorithm for identification and lengthening of partial cDNA sequences with altered expression pattern

2.1. Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 39 was found which occurs 21x more heavily in normal breast tissue than in tumor tissue.

The possible function of this gene region relates to human alpha-B-crystalline.

The result is as follows:

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Electronic Northern for SEQ. ID NO.: 39

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0139	0.0102	1.3639 0.7332
Breast	0.0919	0.0044	21.0995 0.0474
Ovary	0.0091	0.0104	0.8765 1.1409
Endocrine tissue	0.0146	0.0027	5.3582 0.1866
Gastrointestinal	0.0213	0.0048	4.4784 0.2233
Brain	0.1941	0.1358	1.4296 0.6995
Hematopoietic	0.0056	0.0000	undef 0.0000
Skin	0.0995	0.0000	undef 0.0000
Hepatic	0.0050	0.0000	undef 0.0000
Heart	0.2405	0.0000	undef 0.0000
Testicles	0.0061	0.0000	undef 0.0000
Lungs	0.0324	0.0142	2.2824 0.4381
Stomach-esophagus	0.0097	0.0230	0.4200 2.3811
Muscle-skeleton	0.1456	0.0180	8.0893 0.1236
Kidneys	0.0327	0.1643	0.1990 5.0254
Pancreas	0.0038	0.0055	0.6857 1.4584
Penis	0.0539	0.0000	undef 0.0000
Prostate	0.0238	0.0149	1.5980 0.6258
Uterus	0.0363	0.0356	1.0212 0.9793
Breast hyperplasia	0.0291		
Small intestine	0.0156		
Prostatic hyperplasia	0.0119		
Seminal vesicles	0.0178		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.1063
Lungs	0.0074
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0419

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.2925
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0379
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0874
Testicles	0.0234
Lungs	0.0082
Nerves	0.0462
Prostate	0.0321
Sensory organs	0.0542

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2.1.2

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 41 was found which occurs 15x more heavily in normal breast tissue than in tumor tissue.

The possible function of this gene region relates to human extracellular protein S1-5.

The result is as follows:

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Electronic Northern for SEQ. ID NO.: 41

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0186	0.0026	7.2739 0.1375
Breast	0.0666	0.0044	15.2895 0.0654
Ovary	0.0000	0.0026	0.0000 undef
Endocrine tissue	0.0347	0.0436	0.7954 1.2573
Gastrointestinal	0.0078	0.0095	0.8143 1.2281
Brain	0.0288	0.0077	3.7599 0.2660
Hematopoietic	0.0028	0.0000	undef 0.0000
Skin	0.0497	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0498	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0125	0.0095	1.3168 0.7594
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0086	0.0420	0.2039 4.9036
Kidneys	0.0178	0.0000	undef 0.0000
Pancreas	0.0038	0.0000	undef 0.0000
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus	0.0000	0.0000	undef undef
Breast hyperplasia	0.0000	0.0000	undef undef
Small intestine	0.0799		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0089		
White blood cells	0.0000		
	0.0070		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0313
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0099
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0156
Lungs	0.0000
Nerves	0.0120
Prostate	0.0000
Sensory organs	0.0000

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2.1.3

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 42 was found which occurs 12x more heavily in normal breast tissue than in tumor tissue.

The possible function of this gene region relates to secreted "frizzled-related protein."

The result is as follows:

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Electronic Northern for SEQ. ID NO.: 42

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0511	0.0026	20.00330.0500
Breast	0.0533	0.0044	12.23160.0818
Ovary	0.0030	0.0078	0.3895 2.5671
Endocrine tissue	0.0128	0.0027	4.6885 0.2133
Gastrointestinal	0.0039	0.0000	undef 0.0000
Brain	0.0059	0.0099	0.6021 1.6609
Hematopoietic	0.0014	0.0000	undef 0.0000
Skin	0.0348	0.0000	undef 0.0000
Hepatic	0.0149	0.0065	2.2954 0.4356
Heart	0.0085	0.0000	undef 0.0000
Testicles	0.0061	0.0117	0.5224 1.9144
Lungs	0.0025	0.0000	undef 0.0000
Stomach-esophagus	0.0097	0.0000	undef 0.0000
Muscle-skeleton	0.0120	0.0240	0.4996 2.0015
Kidneys	0.0535	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0090	0.0000	undef 0.0000
Prostate	0.0048	0.0085	0.5593 1.7879
Uterus	0.0231	0.0000	undef 0.0000
Breast hyperplasia	0.1126		
Small intestine	0.0156		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0178		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0615
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0573
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0249
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Ovary-uterus	0.0205
Endocrine tissue	0.0000
Fetal	0.0117
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0161
Sensory organs	0.0000
	0.0000

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In an analogous procedure, the following Northernblots were also found:

Electronic Northern Blot for SEQ. ID. NO: 1

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0139	0.0179	0.7793 1.2831
	0.0160	0.0022	7.3390 0.1363
Bladder	0.0030	0.0052	0.5843 1.7114
Breast	0.0036	0.0109	0.3349 2.9861
Ovary	0.0039	0.0238	0.1629 6.1405
Endocrine tissue	0.0102	0.0088	1.1612 0.8612
Gastrointestinal	0.0070	0.0000	undef 0.0000
Brain	0.0050	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0065	0.0000 undef
Skin	0.0011	0.0137	0.0771 12.9744
Hepatic	0.0122	0.0117	1.0447 0.9572
Heart	0.0037	0.0071	0.5267 1.8986
Testicles	0.0000	0.0000	undef undef
Lungs	0.0103	0.0120	0.8565 1.1675
Stomach-esophagus	0.0030	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0110	0.0000 undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0048	0.0128	0.3729 2.6818
Penis	0.0066	0.0000	undef 0.0000
Prostate	0.0109		
Uterus	0.0000		
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0089		
Sensory organs	0.0000		
White blood cells	0.0061		

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0154
Brain	0.0313
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0371
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0244
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0078
Lungs	0.0000
Nerves	0.0020
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 2

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0080	0.0000	undef 0.0000
Breast	0.0000	0.0052	0.0000 undef
Ovary	0.0036	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0143	0.0000 undef
Gastrointestinal	0.0093	0.0044	2.1288 0.4698
Brain	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0099	0.0000	undef 0.0000
Skin	0.0000	0.0065	0.0000 undef
Hepatic	0.0032	0.0000	undef 0.0000
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0037	0.0024	1.5801 0.6329
Lungs	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0017	0.0000	undef 0.0000
Muscle-skeleton	0.0030	0.0068	0.4342 2.3033
Kidneys	0.0019	0.0000	undef 0.0000
Pancreas	0.0060	0.0000	undef 0.0000
Penis	0.0071	0.0064	1.1186 0.8939
Prostate	0.0050	0.0000	undef 0.0000
Uterus	0.0036		
Breast hyperplasia	0.0093		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0044		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0205
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0082
Nerves	0.0050
Prostate	0.0000
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 3

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0000	undef 0.0000
Breast	0.1066	0.0065	16.308 0.0613
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0000	0.0000	undef undef
Brain	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0056	0.0000	undef 0.0000
Skin	0.0448	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0095	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidneys	0.0059	0.0000	undef 0.0000
Pancreas	0.0038	0.0000	undef 0.0000
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0021	0.0000 undef
Uterus	0.0000	0.0000	undef undef
Breast hyperplasia	0.0400		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		
	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

000260 69594960

Electronic Northern Blot for SEQ. ID. NO: 4

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0133	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0018	0.0054	0.3349	2.9861
Endocrine tissue	0.0078	0.0048	1.6285	0.6141
Gastrointestinal	0.0034	0.0022	1.5482	0.6459
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0099	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0061	0.0000	undef	0.0000
Testicles	0.0025	0.0024	1.0534	0.9493
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0060	0.0000	undef
Muscle-skeleton	0.0089	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0024	0.0021	1.1186	0.8939
Prostate	0.0033	0.0214	0.1547	6.4632
Uterus	0.0073			
Breast hyperplasia	0.0000			
Small intestine	0.0059			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0064
Sensory organs	0.0155

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 5

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0790	0.0435	1.8185	0.5499
Bladder	0.0187	0.0022	8.5621	0.1168
Breast	0.0122	0.0000	undef	0.0000
Ovary	0.0000	0.0027	0.0000	undef
Endocrine tissue	0.0329	0.0000	undef	0.0000
Gastrointestinal	0.0085	0.0033	2.5804	0.3875
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0212	0.0000	undef	0.0000
Heart	0.0122	0.0117	1.0447	0.9572
Testicles	0.0025	0.0071	0.3511	2.8478
Lungs	0.1159	0.0383	3.0238	0.3307
Stomach-esophagus	0.0240	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0019	0.0000	undef	0.0000
Pancreas	0.0898	0.0000	undef	0.0000
Penis	0.0262	0.0192	1.3672	0.7314
Prostate	0.0099	0.0427	0.2321	4.3088
Uterus	0.0291			
Breast hyperplasia	0.0530			
Small intestine	0.0178			
Prostatic hyperplasia	0.0445			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0064
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 10

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0107	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0027	0.0000	undef
Endocrine tissue	0.0039	0.0000	undef	0.0000
Gastrointestinal	0.0025	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0099	0.0000	undef	0.0000
Skin	0.0000	0.0065	0.0000	undef
Hepatic	0.0021	0.0000	undef	0.0000
Heart	0.0061	0.0000	undef	0.0000
Testicles	0.0025	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0017	0.0000	undef	0.0000
Muscle-skeleton	0.0059	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0476
Ovary-uterus	0.0000
Endocrine tissue	0.0245
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0000
Nerves	0.0080
Prostate	0.0000
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 11

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0067	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0073	0.0054	1.3396	0.7465
Gastrointestinal	0.0000	0.0048	0.0000	undef
Brain	0.0144	0.0110	1.3160	0.7599
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lungs	0.0025	0.0095	0.2634	3.7971
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5710	1.7513
Kidneys	0.0030	0.0000	undef	0.0000
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0048	0.0149	0.3196	3.1288
Uterus	0.0033	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0093			
Prostatic hyperplasia	0.0149			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0091
Endocrine tissue	0.0245
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0080
Prostate	0.0128
Sensory organs	0.0000

000260" 69594569

Electronic Northern Blot for SEQ. ID. NO: 12

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0093	0.0022	4.2811	0.2336
Breast	0.0000	0.0104	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0024	1.5801	0.6329
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0030	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0024	0.0000	undef	0.0000
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0073			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0245
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0000
Sensory organs	0.0232

000260 0954560

Electronic Northern Blot for SEQ. ID. NO: 13

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0000	undef 0.0000
	0.0080	0.0022	3.6695 0.2725
Bladder	0.0091	0.0000	undef 0.0000
Breast	0.0128	0.0054	2.3442 0.4266
Ovary	0.0000	0.0048	0.0000 undef
Endocrine tissue	0.0042	0.0022	1.9353 0.5167
Gastrointestinal	0.0014	0.0000	undef 0.0000
Brain	0.0050	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0032	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0012	0.0024	0.5267 1.8986
Testicles	0.0000	0.0000	undef undef
Lungs	0.0051	0.0060	0.8565 1.1675
Stomach-esophagus	0.0030	0.0137	0.2171 4.6066
Muscle-skeleton	0.0000	0.0055	0.0000 undef
Kidneys	0.0030	0.0000	undef 0.0000
Pancreas	0.0048	0.0000	undef 0.0000
Penis	0.0083	0.0356	0.2321 4.3088
Prostate	0.0073		
Uterus	0.0125		
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0044		

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0092
Brain	0.0063
Hematopoietic	0.0079
Heart-blood vessels	0.0164
Lungs	0.0074
Kidneys	0.0185
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0128
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0010
Prostate	0.0064
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 14

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0046	0.0051	0.9092 1.0998
Bladder	0.0120	0.0000	undef 0.0000
Breast	0.0000	0.0026	0.0000 undef
Ovary	0.0036	0.0027	1.3396 0.7465
Endocrine tissue	0.0019	0.0000	undef 0.0000
Gastrointestinal	0.0017	0.0022	0.7741 1.2918
Brain	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0042	0.0000	undef 0.0000
Heart	0.0183	0.0000	undef 0.0000
Testicles	0.0012	0.0024	0.5267 1.8986
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0086	0.0000	undef 0.0000
Muscle-skeleton	0.0030	0.0000	undef 0.0000
Kidneys	0.0000	0.0110	0.0000 undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0095	0.0043	2.2373 0.4470
Prostate	0.0017	0.0071	0.2321 4.3088
Uterus	0.0073		
Breast hyperplasia	0.0062		
Small intestine	0.0030		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0026		
White blood cells			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0041
Lungs	0.0074
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0140
Gastrointestinal	0.0000
Hematopoietic	0.0285
Skin-muscle	0.0291
Testicles	0.0000
Lungs	0.0000
Nerves	0.0060
Prostate	0.0064
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 15

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0093	0.0000	undef	0.0000
Bladder	0.0187	0.0022	8.5621	0.1168
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0076	0.0011	6.9669	0.1435
Brain	0.0042	0.0000	undef	0.0000
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0053	0.0137	0.3854	2.5949
Heart	0.0000	0.0000	undef	undef
Testicles	0.0025	0.0071	0.3511	2.8478
Lungs	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0059	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0024	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0036			
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0185
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0040
Prostate	0.0000
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 16

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0051	1.8185	0.5499
Breast	0.0160	0.0000	undef	0.0000
Ovary	0.0091	0.0000	undef	0.0000
Endocrine tissue	0.0018	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0017	0.0011	1.5482	0.6459
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5710	1.7513
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0024	0.0000	undef	0.0000
Uterus	0.0099	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0558

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0064
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0064
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 18

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0232	0.0026	9.0924 0.1100
Breast	0.0306	0.0044	7.0332 0.1422
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0027	0.0000 undef
Gastrointestinal	0.0252	0.0000	undef 0.0000
Brain	0.0017	0.0011	1.5482 0.6459
Hematopoietic	0.0042	0.0000	undef 0.0000
Skin	0.0249	0.0000	undef 0.0000
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0148	0.0000	undef 0.0000
Testicles	0.0061	0.0000	undef 0.0000
Lungs	0.0037	0.0024	1.5801 0.6329
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0274	0.0000	undef 0.0000
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0057	0.0000	undef 0.0000
Penis	0.0120	0.0267	0.4492 2.2260
Prostate	0.0095	0.0000	undef 0.0000
Uterus	0.0132	0.0000	undef 0.0000
Breast hyperplasia	0.0291		
Small intestine	0.0062		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0000		
Sensory organs	0.0118		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 19

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0000	undef	0.0000
Breast	0.0120	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0054	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0017	0.0011	1.5482	0.6459
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0074	0.0275	0.2698	3.7070
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidneys	0.0030	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0048	0.0000	undef	0.0000
Uterus	0.0033	0.0000	undef	0.0000
Breast hyperplasia	0.0073			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0140
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

000260" 6954950

Electronic Northern Blot for SEQ. ID. NO: 21

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0227	0.0044	5.1984 0.1924
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0019	0.0095	0.2036 4.9124
Brain	0.0017	0.0000	undef 0.0000
Hematopoietic	0.0042	0.0000	undef 0.0000
Skin	0.0149	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0064	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0012	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0153	0.0000 undef
Muscle-skeleton	0.0017	0.0060	0.2855 3.5025
Kidneys	0.0059	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus	0.0000	0.0000	undef undef
Breast hyperplasia	0.0000	0.0000	undef undef
Small intestine	0.0036		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		
	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0544
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0064
Sensory organs	0.0000

000260 " 69594960

Electronic Northern Blot for SEQ. ID. NO: 22

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0133	0.0000	undef 0.0000
Breast	0.0000	0.0000	undef undef
Ovary	0.0018	0.0000	undef 0.0000
Endocrine tissue	0.0058	0.0000	undef 0.0000
Gastrointestinal	0.0000	0.0033	0.0000 undef
Brain	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lungs	0.0050	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0034	0.0060	0.5710 1.7513
Kidneys	0.0030	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0024	0.0064	0.3729 2.6818
Uterus	0.0017	0.0000	undef 0.0000
Breast hyperplasia	0.0109		
Small intestine	0.0000		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

000260 69594960

Electronic Northern Blot for SEQ. ID. NO: 23

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0046	0.0026	1.8185	0.5499
	0.0133	0.0022	6.1158	0.1635
Bladder	0.0000	0.0000	undef	undef
Breast	0.0036	0.0027	1.3396	0.7465
Ovary	0.0097	0.0000	undef	0.0000
Endocrine tissue	0.0008	0.0033	0.2580	3.8754
Gastrointestinal	0.0014	0.0000	undef	0.0000
Brain	0.0050	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0011	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0037	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0069	0.0060	1.1420	0.8756
Stomach-esophagus	0.0149	0.0000	undef	0.0000
Muscle-skeleton	0.0038	0.0000	undef	0.0000
Kidneys	0.0030	0.0000	undef	0.0000
Pancreas	0.0024	0.0000	undef	0.0000
Penis	0.0033	0.0071	0.4642	2.1544
Prostate	0.0036			
Uterus	0.0000			
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0118			
Sensory organs	0.0000			
White blood cells				

FETUS
% freq.

	0.0000
Development	0.0031
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0041
Heart-blood vessels	0.0037
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0136
Breast	0.0046
Ovary-uterus	0.0490
Endocrine tissue	0.0198
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0192
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 24

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0139	0.0153	0.9092 1.0998
Breast	0.0173	0.0022	7.9505 0.1258
Ovary	0.0000	0.0026	0.0000 undef
Endocrine tissue	0.0018	0.0027	0.6698 1.4930
Gastrointestinal	0.0058	0.0000	undef 0.0000
Brain	0.0085	0.0142	0.5955 1.6794
Hematopoietic	0.0042	0.0000	undef 0.0000
Skin	0.0298	0.0000	undef 0.0000
Hepatic	0.0050	0.0000	undef 0.0000
Heart	0.0106	0.0000	undef 0.0000
Testicles	0.0061	0.0000	undef 0.0000
Lungs	0.0037	0.0071	0.5267 1.8986
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0103	0.0000	undef 0.0000
Kidneys	0.0178	0.0068	2.6050 0.3839
Pancreas	0.0019	0.0055	0.3428 2.9168
Penis	0.0000	0.0533	0.0000 undef
Prostate	0.0048	0.0021	2.2373 0.4470
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0327		
Small intestine	0.0062		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0089		
Sensory organs	0.0118		
White blood cells	0.0244		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0000
Nerves	0.0050
Prostate	0.0000
Sensory organs	0.0000

000260" 69594560

Electronic Northern Blot for SEQ. ID. NO: 25

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0651	0.0204	3.1823 0.3142
Breast	0.0400	0.0065	6.1158 0.1635
Ovary	0.0213	0.0026	8.1803 0.1222
Endocrine tissue	0.0109	0.0163	0.6698 1.4930
Gastrointestinal	0.0271	0.0000	undef 0.0000
Brain	0.0119	0.0066	1.8062 0.5536
Hematopoietic	0.0196	0.0000	undef 0.0000
Skin	0.0199	0.0000	undef 0.0000
Hepatic	0.0050	0.0065	0.7651 1.3069
Heart	0.0286	0.0000	undef 0.0000
Testicles	0.0061	0.0000	undef 0.0000
Lungs	0.0174	0.0047	3.6870 0.2712
Stomach-esophagus	0.0193	0.0077	2.5198 0.3968
Muscle-skeleton	0.0206	0.0120	1.7130 0.5838
Kidneys	0.0089	0.0068	1.3025 0.7678
Pancreas	0.0019	0.0000	undef 0.0000
Penis	0.0599	0.0000	undef 0.0000
Prostate	0.0214	0.0362	0.5922 1.6886
Uterus	0.0430	0.0000	undef 0.0000
Breast hyperplasia	0.0254		
Small intestine	0.0343		
Prostatic hyperplasia	0.0297		
Seminal vesicles	0.0356		
Sensory organs	0.0118		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0197
Heart-blood vessels	0.0041
Lungs	0.0185
Kidneys	0.0309
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0816
Ovary-uterus	0.0160
Endocrine tissue	0.0000
Fetal	0.0105
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0040
Prostate	0.0385
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 26

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0187	0.0022	8.5621	0.1168
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0110	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Small intestine	0.0036			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

000260" 6994960

Electronic Northern Blot for SEQ. ID. NO: 28

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0102	0.9092 1.0998
Bladder	0.0267	0.0087	3.0579 0.3270
Breast	0.0091	0.0156	0.5843 1.7114
Ovary	0.0128	0.0082	1.5628 0.6399
Endocrine tissue	0.0174	0.0095	1.8321 0.5458
Gastrointestinal	0.0127	0.0153	0.8294 1.2057
Brain	0.0042	0.0000	undef 0.0000
Hematopoietic	0.0149	0.0000	undef 0.0000
Skin	0.0149	0.0194	0.7651 1.3069
Hepatic	0.0085	0.0137	0.6166 1.6218
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0212	0.0189	1.1193 0.8934
Lungs	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0240	0.0120	1.9985 0.5004
Muscle-skeleton	0.0119	0.0000	undef 0.0000
Kidneys	0.0114	0.0166	0.6857 1.4584
Pancreas	0.0090	0.0267	0.3369 2.9680
Penis	0.0191	0.0298	0.6392 1.5644
Prostate	0.0149	0.0000	undef 0.0000
Uterus	0.0109		
Breast hyperplasia	0.0093		
Small intestine	0.0178		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0113		
White blood cells			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0247
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0160
Endocrine tissue	0.0490
Fetal	0.0245
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles	0.0000
Lungs	0.0164
Nerves	0.0211
Prostate	0.0256
Sensory organs	0.0000

000260" 69594460

Electronic Northern Blot for SEQ. ID. NO: 29

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0179	0.0000 undef
Bladder	0.0466	0.0131	3.5675 0.2803
Breast	0.0304	0.0130	2.3372 0.4279
Ovary	0.0237	0.0300	0.7916 1.2633
Endocrine tissue	0.0136	0.0238	0.5700 1.7544
Gastrointestinal	0.0424	0.0263	1.6127 0.6201
Brain	0.0070	0.0000	undef 0.0000
Hematopoietic	0.0348	0.0000	undef 0.0000
Skin	0.0198	0.0065	3.0606 0.3267
Hepatic	0.0265	0.0687	0.3854 2.5949
Heart	0.0244	0.0000	undef 0.0000
Testicles	0.0336	0.0236	1.4221 0.7032
Lungs	0.0483	0.0307	1.5749 0.6350
Stomach-esophagus	0.0154	0.0240	0.6424 1.5567
Muscle-skeleton	0.0119	0.0274	0.4342 2.3033
Kidneys	0.0133	0.0166	0.8000 1.2501
Pancreas	0.0359	0.0000	undef 0.0000
Penis	0.0095	0.0170	0.5593 1.7879
Prostate	0.0132	0.0000	undef 0.0000
Uterus	0.0291		
Breast hyperplasia	0.0187		
Small intestine	0.0149		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0118		
Sensory organs	0.0052		
White blood cells			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0277
Brain	0.0188
Hematopoietic	0.0236
Heart-blood vessels	0.0368
Lungs	0.0407
Kidneys	0.0309
Prostate	0.0249
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0228
Endocrine tissue	0.0245
Fetal	0.0280
Gastrointestinal	0.0122
Hematopoietic	0.0171
Skin-muscle	0.0648
Testicles	0.0156
Lungs	0.0246
Nerves	0.0221
Prostate	0.0192
Sensory organs	0.1393

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	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0093	0.0026	3.6370	0.2750
Bladder	0.0040	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0036	0.0082	0.4465	2.2395
Endocrine tissue	0.0019	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0120	0.0000	undef
Brain	0.0028	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0053	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0000	undef	0.0000
Lungs	0.0193	0.0077	2.5198	0.3968
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0019	0.0055	0.3428	2.9168
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0048	0.0085	0.5593	1.7879
Prostate	0.0033	0.0000	undef	0.0000
Uterus	0.0073			
Breast hyperplasia	0.0062			
Small intestine	0.0000			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0136
Ovary-uterus	0.0114
Endocrine tissue	0.0000
Fetal	0.0087
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0156
Lungs	0.0000
Nerves	0.0040
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 31

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0026	3.6370 0.2750
Bladder	0.0293	0.0087	3.3637 0.2973
Breast	0.0091	0.0156	0.5843 1.7114
Ovary	0.0091	0.0054	1.6745 0.5972
Endocrine tissue	0.0155	0.0190	0.8143 1.2281
Gastrointestinal	0.0008	0.0077	0.1106 9.0427
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0249	0.0000	undef 0.0000
Skin	0.0050	0.0194	0.2550 3.9208
Hepatic	0.0053	0.0550	0.0963 10.3795
Heart	0.0000	0.0000	undef undef
Testicles	0.0075	0.0071	1.0534 0.9493
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0188	0.0060	3.1406 0.3184
Muscle-skeleton	0.0119	0.0000	undef 0.0000
Kidneys	0.0095	0.0276	0.3428 2.9168
Pancreas	0.0120	0.0000	undef 0.0000
Penis	0.0119	0.0128	0.9322 1.0727
Prostate	0.0116	0.0000	undef 0.0000
Uterus	0.0145		
Breast hyperplasia	0.0093		
Small intestine	0.0059		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0470		
Sensory organs	0.0009		
White blood cells			

	FETUS % freq.
Development	0.0154
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0164
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0000

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0068
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0105
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0192
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 32

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0139	0.0077	1.8185 0.5499
Bladder	0.0227	0.0044	5.1984 0.1924
Breast	0.0030	0.0156	0.1948 5.1343
Ovary	0.0109	0.0054	2.0093 0.4977
Endocrine tissue	0.0136	0.0143	0.9500 1.0527
Gastrointestinal	0.0059	0.0033	1.8062 0.5536
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0064	0.0137	0.4624 2.1624
Heart	0.0366	0.0000	undef 0.0000
Testicles	0.0050	0.0000	undef 0.0000
Lungs	0.0000	0.0307	0.0000 undef
Stomach-esophagus	0.0120	0.0000	undef 0.0000
Muscle-skeleton	0.0030	0.0000	undef 0.0000
Kidneys	0.0038	0.0055	0.6857 1.4584
Pancreas	0.0210	0.0000	undef 0.0000
Penis	0.0024	0.0106	0.2237 4.4697
Prostate	0.0050	0.0000	undef 0.0000
Uterus	0.0073		
Breast hyperplasia	0.0218		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0035		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0000
Hematopoietic	0.0285
Skin-muscle	0.0000
Testicles	0.0156
Lungs	0.0164
Nerves	0.0100
Prostate	0.0256
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 33

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0126	0.7274 1.3748
	0.0200	0.0044	4.5868 0.2180
Bladder	0.0091	0.0078	1.1686 0.8557
Breast	0.0018	0.0191	0.0957 10.4512
Ovary	0.0116	0.0000	undef 0.0000
Endocrine tissue	0.0110	0.0197	0.5591 1.7887
Gastrointestinal	0.0070	0.0000	undef 0.0000
Brain	0.0099	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0021	0.0137	0.1541 6.4872
Hepatic	0.0061	0.0117	0.5224 1.9144
Heart	0.0075	0.0118	0.6321 1.5821
Testicles	0.0193	0.0000	undef 0.0000
Lungs	0.0017	0.0240	0.0714 14.0102
Stomach-esophagus	0.0149	0.0000	undef 0.0000
Muscle-skeleton	0.0019	0.0055	0.3428 2.9168
Kidneys	0.0060	0.0000	undef 0.0000
Pancreas	0.0238	0.0192	1.2429 0.8046
Penis	0.0116	0.0000	undef 0.0000
Prostate	0.0036		
Uterus	0.0125		
Breast hyperplasia	0.0059		
Small intestine	0.0178		
Prostatic hyperplasia	0.0118		
Seminal vesicles	0.0061		
Sensory organs			
White blood cells			

FETUS
% freq.

	0.0000
Development	0.0092
Gastrointestinal	0.0000
Brain	0.0157
Hematopoietic	0.0000
Heart-blood vessels	0.0074
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0136
Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0192
Fetal	0.0000
Gastrointestinal	0.0114
Hematopoietic	0.0097
Skin-muscle	0.0234
Testicles	0.0000
Lungs	0.0131
Nerves	0.0064
Prostate	0.0000
Sensory organs	

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 34

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0147	0.0022	6.7274	0.1486
Ovary	0.0091	0.0052	1.7529	0.5705
Endocrine tissue	0.0000	0.0027	0.0000	undef
Gastrointestinal	0.0000	0.0048	0.0000	undef
Brain	0.0008	0.0000	undef	0.0000
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0033	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0000
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 35

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0227	0.0022	10.3969	0.0962
Breast	0.0030	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 36

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0325	0.0077	4.2431 0.2357
Breast	0.0386	0.0065	5.9119 0.1691
Ovary	0.0122	0.0000	undef 0.0000
Endocrine tissue	0.0036	0.0027	1.3396 0.7465
Gastrointestinal	0.0058	0.0048	1.2214 0.8187
Brain	0.0110	0.0033	3.3545 0.2981
Hematopoietic	0.0140	0.0000	undef 0.0000
Skin	0.0149	0.0000	undef 0.0000
Hepatic	0.0099	0.0065	1.5303 0.6535
Heart	0.0085	0.0000	undef 0.0000
Testicles	0.0122	0.0000	undef 0.0000
Lungs	0.0112	0.0000	undef 0.0000
Stomach-esophagus	0.0193	0.0230	0.8399 1.1905
Muscle-skeleton	0.0137	0.0000	undef 0.0000
Kidneys	0.0000	0.0068	0.0000 undef
Pancreas	0.0019	0.0110	0.1714 5.8337
Penis	0.0120	0.0000	undef 0.0000
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0165	0.0071	2.3208 0.4309
Breast hyperplasia	0.0036		
Small intestine	0.0000		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0544
Ovary-uterus	0.0114
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0060
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 37

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0046	0.0077	0.6062	1.6497
Bladder	0.1053	0.0131	8.0525	0.1242
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0058	0.0048	1.2214	0.8187
Gastrointestinal	0.0059	0.0000	undef	0.0000
Brain	0.0084	0.0000	undef	0.0000
Hematopoietic	0.0348	0.0000	undef	0.0000
Skin	0.0099	0.0000	undef	0.0000
Hepatic	0.0201	0.0000	undef	0.0000
Heart	0.0061	0.0000	undef	0.0000
Testicles	0.0012	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0223	0.0240	0.9279	1.0777
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0019	0.0000	undef	0.0000
Pancreas	0.0120	0.0000	undef	0.0000
Penis	0.0024	0.0043	0.5593	1.7879
Prostate	0.0083	0.0000	undef	0.0000
Uterus	0.0618			
Breast hyperplasia	0.0093			
Small intestine	0.0000			
Prostatic hyperplasia	0.0178			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.1632
Ovary-uterus	0.0000
Endocrine tissue	0.0490
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 38

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0026	0.0000 undef
Breast	0.0227	0.0044	5.1984 0.1924
Ovary	0.0000	0.0052	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0039	0.0048	0.8143 1.2281
Brain	0.0000	0.0099	0.0000 undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0099	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0085	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0037	0.0047	0.7901 1.2657
Stomach-esophagus	0.0097	0.0000	undef 0.0000
Muscle-skeleton	0.0154	0.0060	2.5696 0.3892
Kidneys	0.0000	0.0068	0.0000 undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0191	0.0043	4.4745 0.2235
Uterus	0.0017	0.0427	0.0387 25.8527
Breast hyperplasia	0.0036		
Small intestine	0.0125		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0118		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0185
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0020
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 40

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0325	0.0051	6.3647 0.1571
Bladder	0.0267	0.0065	4.0772 0.2453
Breast	0.0030	0.0026	1.1686 0.8557
Ovary	0.0146	0.0000	undef 0.0000
Endocrine tissue	0.0039	0.0095	0.4071 2.4562
Gastrointestinal	0.0068	0.0307	0.2212 4.5213
Brain	0.0028	0.0378	0.0739 13.5274
Hematopoietic	0.0149	0.0000	undef 0.0000
Skin	0.0198	0.0129	1.5303 0.6535
Hepatic	0.1303	0.3299	0.3950 2.5316
Heart	0.0183	0.0351	0.5224 1.9144
Testicles	0.0174	0.0118	1.4748 0.6781
Lungs	0.0097	0.0460	0.2100 4.7622
Stomach-esophagus	0.0188	0.0300	0.6281 1.5921
Muscle-skeleton	0.0119	0.0479	0.2481 4.0308
Kidneys	0.0057	0.0055	1.0285 0.9723
Pancreas	0.0180	0.0267	0.6739 1.4840
Penis	0.0143	0.0021	6.7118 0.1490
Prostate	0.0149	0.0000	undef 0.0000
Uterus	0.0327		
Breast hyperplasia	0.0093		
Small intestine	0.0208		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.1058		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0977

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0408
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0246
Nerves	0.0090
Prostate	0.0000
Sensory organs	0.0852

000260" 69594950

Electronic Northern Blot for SEQ. ID. NO: 43

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0051	0.0000 undef
Bladder	0.0253	0.0044	5.8100 0.1721
Breast	0.0152	0.0338	0.4495 2.2249
Ovary	0.0109	0.0054	2.0093 0.4977
Endocrine tissue	0.0097	0.0000	undef 0.0000
Gastrointestinal	0.0136	0.0044	3.0964 0.3230
Brain	0.0098	0.0000	undef 0.0000
Hematopoietic	0.0099	0.0000	undef 0.0000
Skin	0.0000	0.0065	0.0000 undef
Hepatic	0.0021	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0062	0.0024	2.6336 0.3797
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0051	0.0000	undef 0.0000
Muscle-skeleton	0.0030	0.0068	0.4342 2.3033
Kidneys	0.0019	0.0110	0.1714 5.8337
Pancreas	0.0090	0.0000	undef 0.0000
Penis	0.0095	0.0064	1.4915 0.6705
Prostate	0.0083	0.0000	undef 0.0000
Uterus	0.0036		
Breast hyperplasia	0.0093		
Small intestine	0.0089		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0096		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0188
Hematopoietic	0.0079
Heart-blood vessels	0.0082
Lungs	0.0111
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0099
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles	0.0000
Lungs	0.0000
Nerves	0.0070
Prostate	0.0064
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 45

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0200	0.0022	9.1737	0.1090
Breast	0.0000	0.0026	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0058	0.0048	1.2214	0.8187
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0056	0.0000	undef	0.0000
Hematopoietic	0.0249	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0064	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0038	0.0055	0.6857	1.4584
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0254			
Small intestine	0.0125			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 47

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0051	0.0000	undef
	0.0133	0.0000	undef	0.0000
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Ovary	0.0019	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0062	0.0000	undef	0.0000
Lungs	0.0193	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0024	0.0021	1.1186	0.8939
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0235			
White blood cells	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES

	% frequency
Breast	0.0068
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 48

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0186	0.0077	2.4246	0.4124
Bladder	0.0133	0.0000	undef	0.0000
Breast	0.0030	0.0000	undef	0.0000
Ovary	0.0036	0.0027	1.3396	0.7465
Endocrine tissue	0.0019	0.0000	undef	0.0000
Gastrointestinal	0.0017	0.0033	0.5161	1.9377
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0149	0.0000	undef	0.0000
Skin	0.0149	0.0000	undef	0.0000
Hepatic	0.1494	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0162	0.0000	undef	0.0000
Lungs	0.0097	0.0000	undef	0.0000
Stomach-esophagus	0.0394	0.0000	undef	0.0000
Muscle-skeleton	0.0030	0.0000	undef	0.0000
Kidneys	0.0038	0.0000	undef	0.0000
Pancreas	0.0150	0.0000	undef	0.0000
Penis	0.0024	0.0106	0.2237	4.4697
Prostate	0.0116	0.0142	0.8123	1.2311
Uterus	0.0036			
Breast hyperplasia	0.0093			
Small intestine	0.0030			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.1472
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0408
Ovary-uterus	0.0274
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0234
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

000220" 6954960

Electronic Northern Blot for SEQ. ID. NO: 49

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0186	0.0077	2.4246 0.4124
Bladder	0.0293	0.0087	3.3637 0.2973
Breast	0.0091	0.0234	0.3895 2.5671
Ovary	0.0091	0.0327	0.2791 3.5833
Endocrine tissue	0.0116	0.0143	0.8143 1.2281
Gastrointestinal	0.0110	0.0110	1.0063 0.9937
Brain	0.0112	0.0000	undef 0.0000
Hematopoietic	0.0199	0.0000	undef 0.0000
Skin	0.0149	0.0065	2.2954 0.4356
Hepatic	0.0392	0.0000	undef 0.0000
Heart	0.0122	0.0117	1.0447 0.9572
Testicles	0.0224	0.0071	3.1603 0.3164
Lungs	0.0097	0.0230	0.4200 2.3811
Stomach-esophagus	0.0188	0.0300	0.6281 1.5921
Muscle-skeleton	0.0119	0.0137	0.8683 1.1517
Kidneys	0.0076	0.0000	undef 0.0000
Pancreas	0.0150	0.0267	0.5615 1.7808
Penis	0.0238	0.0128	1.8644 0.5364
Prostate	0.0198	0.0000	undef 0.0000
Uterus	0.0182		
Breast hyperplasia	0.0125		
Small intestine	0.0178		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0252		

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0092
Brain	0.0063
Hematopoietic	0.0157
Heart-blood vessels	0.0245
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0997
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0297
Endocrine tissue	0.0000
Fetal	0.0251
Gastrointestinal	0.0732
Hematopoietic	0.0114
Skin-muscle	0.0615
Testicles	0.0234
Lungs	0.0164
Nerves	0.0171
Prostate	0.0192
Sensory organs	0.0232

000260"69594960

Electronic Northern Blot for SEQ. ID. NO: 50

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0051	0.0000 undef
Bladder	0.0080	0.0000	undef 0.0000
Breast	0.0091	0.0000	undef 0.0000
Ovary	0.0000	0.0109	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0008	0.0033	0.2580 3.8754
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0011	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lungs	0.0075	0.0000	undef 0.0000
Stomach-esophagus	0.0386	0.0000	undef 0.0000
Muscle-skeleton	0.0017	0.0120	0.1428 7.0051
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0019	0.0055	0.3428 2.9168
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0024	0.0043	0.5593 1.7879
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0063
Hematopoietic	0.0079
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Ovary-uterus	0.0091
Endocrine tissue	0.0000
Fetal	0.0227
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 51

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0077	1.2123 0.8249
	0.0133	0.0000	undef 0.0000
Bladder	0.0000	0.0078	0.0000 undef
Breast	0.0018	0.0000	undef 0.0000
Ovary	0.0097	0.0095	1.0178 0.9825
Endocrine tissue	0.0025	0.0099	0.2580 3.8754
Gastrointestinal	0.0084	0.0378	0.2218 4.5091
Brain	0.0099	0.0847	0.1175 8.5131
Hematopoietic	0.0099	0.0065	1.5303 0.6535
Skin	0.0011	0.0000	undef 0.0000
Hepatic	0.0061	0.0000	undef 0.0000
Heart	0.0100	0.0095	1.0534 0.9493
Testicles	0.0000	0.0000	undef undef
Lungs	0.0343	0.0060	5.7101 0.1751
Stomach-esophagus	0.0000	0.0137	0.0000 undef
Muscle-skeleton	0.0000	0.0110	0.0000 undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0071	0.0043	1.6779 0.5960
Penis	0.0033	0.0071	0.4642 2.1544
Prostate	0.0000		
Uterus	0.0062		
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0118		
Sensory organs	0.0209		
White blood cells			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0735
Fetal	0.0140
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 53

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0051	0.0000 undef
Bladder	0.0213	0.0044	4.8926 0.2044
Breast	0.0091	0.0182	0.5008 1.9967
Ovary	0.0091	0.0191	0.4784 2.0902
Endocrine tissue	0.0019	0.0190	0.1018 9.8248
Gastrointestinal	0.0034	0.0066	0.5161 1.9377
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0065	0.0000 undef
Hepatic	0.0106	0.0000	undef 0.0000
Heart	0.0183	0.0000	undef 0.0000
Testicles	0.0075	0.0095	0.7901 1.2657
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0034	0.0000	undef 0.0000
Muscle-skeleton	0.0059	0.0137	0.4342 2.3033
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0150	0.1066	0.1404 7.1232
Penis	0.0119	0.0064	1.8644 0.5364
Prostate	0.0182	0.0071	2.5529 0.3917
Uterus	0.0254		
Breast hyperplasia	0.0093		
Small intestine	0.0059		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0204
Lungs	0.0370
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0087
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lungs	0.0164
Nerves	0.0010
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 54

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0077	1.2123 0.8249
Bladder	0.0200	0.0044	4.5868 0.2180
Breast	0.0152	0.0104	1.4608 0.6846
Ovary	0.0091	0.0054	1.6745 0.5972
Endocrine tissue	0.0039	0.0048	0.8143 1.2281
Gastrointestinal	0.0110	0.0033	3.3545 0.2981
Brain	0.0056	0.0000	undef 0.0000
Hematopoietic	0.0149	0.0000	undef 0.0000
Skin	0.0198	0.0000	undef 0.0000
Hepatic	0.0064	0.0000	undef 0.0000
Heart	0.0122	0.0000	undef 0.0000
Testicles	0.0062	0.0071	0.8779 1.1391
Lungs	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0051	0.0240	0.2141 4.6701
Muscle-skeleton	0.0178	0.0000	undef 0.0000
Kidneys	0.0019	0.0110	0.1714 5.8337
Pancreas	0.0060	0.0000	undef 0.0000
Penis	0.0119	0.0043	2.7966 0.3576
Prostate	0.0050	0.0214	0.2321 4.3088
Uterus	0.0000		
Breast hyperplasia	0.0062		
Small intestine	0.0208		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0540		

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0123
Brain	0.0250
Hematopoietic	0.0275
Heart-blood vessels	0.0082
Lungs	0.0037
Kidneys	0.0185
Prostate	0.0000
Sensory organs	0.0558

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lungs	0.0082
Nerves	0.0040
Prostate	0.0064
Sensory organs	0.0310

09645569.092000

Electronic Northern Blot for SEQ. ID. NO: 56

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0046	0.0000	undef	0.0000
Bladder	0.0227	0.0044	5.1984	0.1924
Breast	0.0000	0.0000	undef	undef
Ovary	0.0018	0.0000	undef	0.0000
Endocrine tissue	0.0058	0.0048	1.2214	0.8187
Gastrointestinal	0.0059	0.0011	5.4187	0.1845
Brain	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0446	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0075	0.0071	1.0534	0.9493
Lungs	0.0097	0.0307	0.3150	3.1748
Stomach-esophagus	0.0120	0.0000	undef	0.0000
Muscle-skeleton	0.0208	0.0068	3.0391	0.3290
Kidneys	0.0038	0.0110	0.3428	2.9168
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0119	0.0106	1.1186	0.8939
Prostate	0.0017	0.0000	undef	0.0000
Uterus	0.0254			
Breast hyperplasia	0.0000			
Small intestine	0.0059			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0383			
White blood cells				

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0118
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0065
Testicles	0.0156
Lungs	0.0082
Nerves	0.0070
Prostate	0.0128
Sensory organs	0.0000

000260" 69594950

Electronic Northern Blot for SEQ. ID. NO: 57

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0120	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

09545569.092000

Electronic Northern Blot for SEQ. ID. NO: 58

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0107	0.0000	undef 0.0000
Breast	0.0213	0.0026	8.1803 0.1222
Ovary	0.0000	0.0054	0.0000 undef
Endocrine tissue	0.0039	0.0000	undef 0.0000
Gastrointestinal	0.0212	0.0077	2.7647 0.3617
Brain	0.0000	0.0378	0.0000 undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0021	0.0000	undef 0.0000
Heart	0.0244	0.0000	undef 0.0000
Testicles	0.0087	0.0047	1.8435 0.5424
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0017	0.0060	0.2855 3.5025
Muscle-skeleton	0.0030	0.0068	0.4342 2.3033
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0060	0.0000	undef 0.0000
Penis	0.0000	0.0021	0.0000 undef
Prostate	0.0033	0.0142	0.2321 4.3088
Uterus	0.0036		
Breast hyperplasia	0.0031		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0009		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0111
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0050
Prostate	0.0000
Sensory organs	0.0155

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Electronic Northern Blot for SEQ. ID. NO: 59

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0133	0.0000	undef 0.0000
Breast	0.0000	0.0104	0.0000 undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0008	0.0011	0.7741 1.2918
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0011	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0025	0.0000	undef 0.0000
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0038	0.0000	undef 0.0000
Penis	0.0000	0.0000	undef undef
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0017	0.0000	undef 0.0000
Breast hyperplasia	0.0036		
Small intestine	0.0031		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0082
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles	0.0156
Lungs	0.0000
Nerves	0.0040
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 60

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0186	0.0051	3.6370 0.2750
Bladder	0.0160	0.0044	3.6695 0.2725
Breast	0.0061	0.0052	1.1686 0.8557
Ovary	0.0201	0.1634	0.1228 8.1438
Endocrine tissue	0.0039	0.0000	undef 0.0000
Gastrointestinal	0.0305	0.0110	2.7868 0.3588
Brain	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef 0.0000
Hepatic	0.0244	0.0275	0.8864 1.1282
Heart	0.0000	0.0000	undef undef
Testicles	0.0050	0.0047	1.0534 0.9493
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0120	0.0060	1.9985 0.5004
Kidneys	0.0000	0.0205	0.0000 undef
Pancreas	0.0000	0.0110	0.0000 undef
Penis	0.0359	0.0000	undef 0.0000
Prostate	0.0119	0.0149	0.7990 1.2515
Uterus	0.0099	0.0071	1.3925 0.7181
Breast hyperplasia	0.0109		
Small intestine	0.0093		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0089		
Sensory organs	0.0353		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0082
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0046
Endocrine tissue	0.0490
Fetal	0.0035
Gastrointestinal	0.0244
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0156
Lungs	0.0082
Nerves	0.0161
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 61

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0046	0.0051	0.9092 1.0998
	0.0306	0.0022	14.0663 0.0711
Bladder	0.0030	0.0078	0.3895 2.5671
Breast	0.0055	0.0027	2.0093 0.4977
Ovary	0.0058	0.0238	0.2443 4.0937
Endocrine tissue	0.0068	0.0022	3.0964 0.3230
Gastrointestinal	0.0014	0.0000	undef 0.0000
Brain	0.0199	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0065	0.0000 undef
Skin	0.0085	0.0000	undef 0.0000
Hepatic	0.0061	0.0000	undef 0.0000
Heart	0.0075	0.0047	1.5801 0.6329
Testicles	0.0000	0.0077	0.0000 undef
Lungs	0.0017	0.0060	0.2855 3.5025
Stomach-esophagus	0.0030	0.0068	0.4342 2.3033
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0060	0.0000	undef 0.0000
Pancreas	0.0024	0.0043	0.5593 1.7879
Penis	0.0033	0.0000	undef 0.0000
Prostate	0.0145		
Uterus	0.0125		
Breast hyperplasia	0.0059		
Small intestine	0.0000		
Prostatic hyperplasia	0.0235		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0128
Sensory organs	0.0155

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Electronic Northern Blot for SEQ. ID. NO: 62

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0120	0.0022	5.5042 0.1817
Breast	0.0030	0.0104	0.2922 3.4228
Ovary	0.0055	0.0027	2.0093 0.4977
Endocrine tissue	0.0058	0.0048	1.2214 0.8187
Gastrointestinal	0.0119	0.0131	0.9031 1.1073
Brain	0.0070	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0065	0.0000 undef
Hepatic	0.0000	0.0137	0.0000 undef
Heart	0.0183	0.0000	undef 0.0000
Testicles	0.0037	0.0024	1.5801 0.6329
Lungs	0.0000	0.0077	0.0000 undef
Stomach-esophagus	0.0017	0.0060	0.2855 3.5025
Muscle-skeleton	0.0030	0.0000	undef 0.0000
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0090	0.0000	undef 0.0000
Penis	0.0024	0.0085	0.2797 3.5758
Prostate	0.0083	0.0142	0.5802 1.7235
Uterus	0.0073		
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0353		
White blood cells	0.0044		

	FETUS % freq.
Development	0.0307
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0245
Fetal	0.0052
Gastrointestinal	0.0000
Hematopoietic	0.0171
Skin-muscle	0.0097
Testicles	0.0078
Lungs	0.0246
Nerves	0.0271
Prostate	0.0192
Sensory organs	0.0000

000260 69994950

Electronic Northern Blot for SEQ. ID. NO: 63

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0232	0.0204	1.1366 0.8799
	0.0267	0.0087	3.0579 0.3270
Bladder	0.0304	0.0130	2.3372 0.4279
Breast	0.0529	0.0735	0.7194 1.3901
Ovary	0.0174	0.0048	3.6642 0.2729
Endocrine tissue	0.0170	0.0208	0.8148 1.2272
Gastrointestinal	0.0070	0.0378	0.1848 5.4110
Brain	0.0199	0.0000	undef 0.0000
Hematopoietic	0.0198	0.0000	undef 0.0000
Skin	0.0180	0.0550	0.3276 3.0528
Hepatic	0.0122	0.0117	1.0447 0.9572
Heart	0.0249	0.0118	2.1069 0.4746
Testicles	0.0386	0.0153	2.5198 0.3968
Lungs	0.0120	0.0180	0.6662 1.5011
Stomach-esophagus	0.0089	0.0068	1.3025 0.7678
Muscle-skeleton	0.0170	0.0055	3.0855 0.3241
Kidneys	0.0509	0.0000	undef 0.0000
Pancreas	0.0357	0.0149	2.3971 0.4172
Penis	0.0297	0.0214	1.3925 0.7181
Prostate	0.0000		
Uterus	0.0093		
Breast hyperplasia	0.0178		
Small intestine	0.0267		
Prostatic hyperplasia	0.0118		
Seminal vesicles	0.0000		
Sensory organs			
White blood cells			

	FETUS % freq.
	0.0154
Development	0.0185
Gastrointestinal	0.0125
Brain	0.0000
Hematopoietic	0.0491
Heart-blood vessels	0.0037
Lungs	0.0432
Kidneys	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES

	% frequency
	0.0272
Breast	0.0342
Ovary-uterus	0.0000
Endocrine tissue	0.0157
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0648
Skin-muscle	0.0312
Testicles	0.0246
Lungs	0.0151
Nerves	0.0192
Prostate	0.0697
Sensory organs	

000260" 6954960

Electronic Northern Blot for SEQ. ID. NO: 64

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0232	0.0102	2.2731 0.4399
Bladder	0.0240	0.0065	3.6695 0.2725
Breast	0.0213	0.0416	0.5113 1.9559
Ovary	0.0237	0.0027	8.7071 0.1148
Endocrine tissue	0.0213	0.0381	0.5598 1.7863
Gastrointestinal	0.0136	0.0099	1.3762 0.7266
Brain	0.0042	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0248	0.0129	1.9129 0.5228
Hepatic	0.0191	0.0137	1.3873 0.7208
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0112	0.0095	1.1851 0.8438
Lungs	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0051	0.0060	0.8565 1.1675
Muscle-skeleton	0.0149	0.0205	0.7236 1.3820
Kidneys	0.0076	0.0055	1.3713 0.7292
Pancreas	0.0269	0.0267	1.0108 0.9893
Penis	0.0333	0.0170	1.9576 0.5108
Prostate	0.0099	0.0071	1.3925 0.7181
Uterus	0.0145		
Breast hyperplasia	0.0343		
Small intestine	0.0178		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0139		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0082
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles	0.0000
Lungs	0.0000
Nerves	0.0110
Prostate	0.0385
Sensory organs	0.0155

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 65

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0139	0.0026	5.4554	0.1833
	0.0093	0.0022	4.2811	0.2336
Bladder	0.0000	0.0130	0.0000	undef
Breast	0.0036	0.0082	0.4465	2.2395
Ovary	0.0000	0.0095	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0028	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0085	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0012	0.0000	undef	0.0000
Testicles	0.0193	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0019	0.0000	undef	0.0000
Kidneys	0.0060	0.0000	undef	0.0000
Pancreas	0.0048	0.0000	undef	0.0000
Penis	0.0066	0.0214	0.3094	3.2316
Prostate	0.0109			
Uterus	0.0093			
Breast hyperplasia	0.0000			
Small intestine	0.0178			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0245
Fetal	0.0070
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0078
Lungs	0.0164
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 66

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0077	0.0000 undef
Bladder	0.0120	0.0022	5.5042 0.1817
Breast	0.0030	0.0052	0.5843 1.7114
Ovary	0.0000	0.0054	0.0000 undef
Endocrine tissue	0.0039	0.0000	undef 0.0000
Gastrointestinal	0.0008	0.0033	0.2580 3.8754
Brain	0.0070	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0053	0.0000	undef 0.0000
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0062	0.0071	0.8779 1.1391
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0019	0.0000	undef 0.0000
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0119	0.0000	undef 0.0000
Prostate	0.0033	0.0071	0.4642 2.1544
Uterus	0.0036		
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0061		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0236
Heart-blood vessels	0.0082
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0078
Lungs	0.0000
Nerves	0.0020
Prostate	0.0000
Sensory organs	0.0000

000260" 6954960

Electronic Northern Blot for SEQ. ID. NO: 67

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0232	0.0051	4.5462 0.2200
Bladder	0.0506	0.0044	11.6200 0.0861
Breast	0.0000	0.0000	undef undef
Ovary	0.0036	0.0000	undef 0.0000
Endocrine tissue	0.0019	0.0000	undef 0.0000
Gastrointestinal	0.0034	0.0000	undef 0.0000
Brain	0.0028	0.0378	0.0739 13.5274
Hematopoietic	0.0348	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0254	0.0137	1.8498 0.5406
Heart	0.0000	0.0000	undef undef
Testicles	0.0025	0.0071	0.3511 2.8478
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0017	0.0240	0.0714 14.0102
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0019	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0024	0.0000	undef 0.0000
Prostate	0.0017	0.0000	undef 0.0000
Uterus	0.0872		
Breast hyperplasia	0.0093		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0044		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0157
Heart-blood vessels	0.0082
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0064
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 68

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0046	0.0077	0.6062 1.6497
Bladder	0.0253	0.0044	5.8100 0.1721
Breast	0.0152	0.0312	0.4869 2.0537
Ovary	0.0146	0.0163	0.8930 1.1198
Endocrine tissue	0.0078	0.0048	1.6285 0.6141
Gastrointestinal	0.0170	0.0110	1.5482 0.6459
Brain	0.0056	0.0378	0.1478 6.7637
Hematopoietic	0.0099	0.0000	undef 0.0000
Skin	0.0050	0.0065	0.7651 1.3069
Hepatic	0.0106	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0050	0.0118	0.4214 2.3732
Lungs	0.0000	0.0077	0.0000 undef
Stomach-esophagus	0.0017	0.0300	0.0571 17.5127
Muscle-skeleton	0.0297	0.0205	1.4472 0.6910
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0180	0.0000	undef 0.0000
Penis	0.0048	0.0085	0.5593 1.7879
Prostate	0.0198	0.0142	1.3925 0.7181
Uterus	0.0327		
Breast hyperplasia	0.0125		
Small intestine	0.0059		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0026		

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0123
Brain	0.0063
Hematopoietic	0.0079
Heart-blood vessels	0.0123
Lungs	0.0259
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0023
Endocrine tissue	0.0245
Fetal	0.0070
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0156
Lungs	0.0082
Nerves	0.0141
Prostate	0.0064
Sensory organs	0.0000

000260" 69554960

Electronic Northern Blot for SEQ. ID. NO: 69

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0120	0.0000	undef	0.0000
Breast	0.0030	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0051	0.0033	1.5482	0.6459
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0024	1.5801	0.6329
Lungs	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0059	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0105
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0100
Prostate	0.0000
Sensory organs	0.0077

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 71

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0232	0.0051	4.5462 0.2200
Breast	0.0173	0.0044	3.9753 0.2516
Ovary	0.0091	0.0000	undef 0.0000
Endocrine tissue	0.0055	0.0163	0.3349 2.9861
Gastrointestinal	0.0039	0.0048	0.8143 1.2281
Brain	0.0034	0.0131	0.2580 3.8754
Hematopoietic	0.0028	0.0000	undef 0.0000
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0000	0.0129	0.0000 undef
Heart	0.0053	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0062	0.0047	1.3168 0.7594
Stomach-esophagus	0.0097	0.0077	1.2599 0.7937
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidneys	0.0119	0.0000	undef 0.0000
Pancreas	0.0076	0.0166	0.4571 2.1876
Penis	0.0150	0.0000	undef 0.0000
Prostate	0.0071	0.0085	0.8390 1.1919
Uterus	0.0165	0.0000	undef 0.0000
Breast hyperplasia	0.0073		
Small intestine	0.0031		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0026		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0123
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0091
Endocrine tissue	0.0000
Fetal	0.0064
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0156
Lungs	0.0246
Nerves	0.0040
Prostate	0.0000
Sensory organs	0.0155

000260" 69594660

Electronic Northern Blot for SEQ. ID. NO: 72

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0107	0.0000	undef 0.0000
Breast	0.0000	0.0026	0.0000 undef
Ovary	0.0000	0.0027	0.0000 undef
Endocrine tissue	0.0078	0.0000	undef 0.0000
Gastrointestinal	0.0017	0.0055	0.3096 3.2295
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0129	0.0000 undef
Hepatic	0.0042	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0012	0.0024	0.5267 1.8986
Lungs	0.0000	0.0153	0.0000 undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0089	0.0000	undef 0.0000
Kidneys	0.0019	0.0000	undef 0.0000
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0095	0.0043	2.2373 0.4470
Prostate	0.0017	0.0071	0.2321 4.3088
Uterus	0.0000		
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0009		

FETUS
% freq.

	0.0000
Development	0.0092
Gastrointestinal	0.0000
Brain	0.0039
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0068
Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0035
Fetal	0.0000
Gastrointestinal	0.0171
Hematopoietic	0.0097
Skin-muscle	0.0000
Testicles	0.0082
Lungs	0.0030
Nerves	0.0128
Prostate	0.0000
Sensory organs	

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 74

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0093	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0018	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0024	0.0000	undef
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0024	0.0000	undef	0.0000
Uterus	0.0083	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0089			
White blood cells	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES

	% frequency
Breast	0.0000
Ovary-uterus	0.0114
Endocrine tissue	0.0245
Fetal	0.0006
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory organs	0.0000

000260" 6954960

Electronic Northern Blot for SEQ. ID. NO: 76

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0153	0.0000 undef
Bladder	0.0080	0.0000	undef 0.0000
Breast	0.0030	0.0078	0.3895 2.5671
Ovary	0.0036	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0190	0.0000 undef
Gastrointestinal	0.0017	0.0033	0.5161 1.9377
Brain	0.0056	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0012	0.0024	0.5267 1.8986
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0069	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0024	0.0021	1.1186 0.8939
Uterus	0.0000	0.0000	undef undef
Breast hyperplasia	0.0000		
Small intestine	0.0031		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0035		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0000
Endocrine tissue	0.0735
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory organs	0.0077

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Electronic Northern for Seq. ID: 161

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0100	0.0136	0.7358 1.3590
Bladder	0.0195	0.0164	1.1854 0.8436
Breast	0.0176	0.0042	4.1747 0.2395
Large intestine	0.0115	0.0142	0.8073 1.2386
Small intestine	0.0055	0.0213	0.2577 3.8812
Ovary	0.0030	0.0095	0.3111 3.2146
Endocrine tissue	0.0048	0.0089	0.5432 1.8409
Brain	0.0104	0.0120	0.8704 1.1489
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0030	0.0137	0.2215 4.5144
Testicles	0.0120	0.0118	1.0178 0.9825
Lung	0.0049	0.0055	0.8770 1.1402
Stomach-esophagus	0.0072	0.0128	0.5668 1.7644
Muscle-skeleton	0.0154	0.0111	1.3917 0.7186
Kidney	0.0045	0.0000	undef 0.0000
Pancreas	0.0017	0.0166	0.0997 10.0282
Prostate	0.0075	0.0104	0.7235 1.3821
T lymphoma	0.0076	0.0448	0.1691 5.9152
Uterus	0.0089	0.0138	0.6426 1.5563
White blood cells	0.0096	0.0000	undef 0.0000
Hematopoietic	0.0094		
Penis	0.0054		
Seminal vesicle	0.0141		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0139
Brain	0.0313
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0371
Placenta	0.0061
Prostate	0.0249
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	
Breast_t	
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0101
Gastrointestinal	0.0000
Hematopoietic	0.0029
Skin-muscle	0.0244
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0084
Nerves	0.0000
Kidney_t	0.0000
Ovary uterus	0.0000
Prostate_n	0.0020
Sensory organs	0.0000
White blood cells	0.0090
	0.0121
	0.0000
	0.0000

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Electronic Northern for Seq. ID: 162

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0078	0.0000	undef 0.0000
Breast	0.0123	0.0042	2.9223 0.3422
Large intestine	0.0096	0.0028	3.3639 0.2973
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0032	0.0195	0.1646 6.0749
Brain	0.0041	0.0040	1.0155 0.9848
Skin	0.0110	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lung	0.0080	0.0000	undef 0.0000
Stomach-esophagus	0.0039	0.0018	2.1049 0.4751
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0051	0.0037	1.3917 0.7186
Pancreas	0.0067	0.0000	undef 0.0000
Prostate	0.0000	0.0000	undef undef
T lymphoma	0.0075	0.0026	2.8941 0.3455
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0059	0.0276	0.2142 4.6688
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0013		
Seminal vesicle	0.0134		
Sensory organs	0.0070		

0.0000
FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
0.0000 % frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0017
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0040
Kidney t	0.0000
Ovary Uterus	0.0180
Prostate n	0.0061
Sensory organs	0.0542
White blood cells	0.0000

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Electronic Northern for Seq. ID: 163

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0000	0.0000	undef	undef
Breast	0.0097	0.0000	undef	0.0000
Large intestine	0.0038	0.0057	0.6728	1.4864
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0024	1.2443	0.8036
Endocrine tissue	0.0000	0.0035	0.0000	undef
Brain	0.0041	0.0030	1.3539	0.7386
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0061	0.0000	undef	0.0000
Testicles	0.0080	0.0000	undef	0.0000
Lung	0.0039	0.0037	1.0524	0.9502
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0103	0.0000	undef	0.0000
Kidney	0.0045	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0028	0.0013	2.1706	0.4607
T lymphoma	0.0025	0.0075	0.3381	2.9576
Uterus	0.0030	0.0000	undef	0.0000
White blood cells	0.0027	0.0000	undef	0.0000
Hematopoietic	0.0000			
Penis	0.0027			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0507
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0680
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0245
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0513
Skin-muscle	0.0130
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0121
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

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Electronic Northern for Seq. ID: 164

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0044	0.0000	undef	0.0000
Large intestine	0.0000	0.0057	0.0000	undef
Small intestine	0.0082	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0080	0.0035	2.2634	0.4418
Brain	0.0168	0.0080	2.1034	0.4754
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0051	0.0000	undef	0.0000
Testicles	0.0040	0.0059	0.6786	1.4737
Lung	0.0029	0.0092	0.3157	3.1673
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0037	0.9278	1.0778
Kidney	0.0045	0.0096	0.4642	2.1540
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0085	0.0091	0.9302	1.0750
T lymphoma	0.0000	0.0149	0.0000	undef
Uterus	0.0030	0.0000	undef	0.0000
White blood cells	0.0027	0.0000	undef	0.0000
Hematopoietic	0.0013			
Penis	0.0054			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FEIUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0185
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES

	% frequency
Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0203
Endocrine tissue	0.0245
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0513
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0090
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0090
Sensory organs	0.0061
White blood cells	0.0000
	0.0000

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Electronic Northern for Seq. ID: 165

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0000	0.0000	undef undef
Breast	0.0106	0.0028	3.7573 0.2662
Large intestine	0.0000	0.0028	0.0000 undef
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0095	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0012	0.0010	1.1605 0.8617
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0010	0.0137	0.0738 13.5431
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0068	0.0018	3.6835 0.2715
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0034	0.0000	undef 0.0000
Pancreas	0.0045	0.0000	undef 0.0000
Prostate	0.0033	0.0000	undef 0.0000
T lymphoma	0.0019	0.0013	1.4470 0.6911
Uterus	0.0076	0.0000	undef 0.0000
White blood cells	0.0030	0.0046	0.6426 1.5563
Hematopoietic	0.0021	0.0000	undef 0.0000
Penis	0.0000		
Seminal vesicle	0.0027		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0245
Fetal	0.0070
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0209
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0080
Kidney t	0.0000
Ovary uterus	0.0090
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0232
	0.0000

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Electronic Northern for Seq. ID: 166

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0000	undef 0.0000
Bladder	0.0078	0.0023	3.3190 0.3013
Breast	0.0202	0.0042	4.8009 0.2083
Large intestine	0.0000	0.0028	0.0000 undef
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0032	0.0106	0.3018 3.3136
Brain	0.0168	0.0020	8.4138 0.1189
Skin	0.0147	0.0000	undef 0.0000
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0132	0.0137	0.9599 1.0418
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0175	0.0148	1.1840 0.8446
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0051	0.0000	undef 0.0000
Kidney	0.0134	0.0048	2.7855 0.3590
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0094	0.0039	2.4117 0.4146
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0080		
Seminal vesicle	0.0268		
Sensory organs	0.0211		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0188
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0247
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0502

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0231
Kidney t	0.0000
Ovary Uterus	0.0000
Prostate n	0.0061
Sensory organs	0.0077
White blood cells	0.0000

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Electronic Northern for Seq. ID: 167

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0141	0.0000	undef	0.0000
Large intestine	0.0019	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0024	1.2443	0.8036
Endocrine tissue	0.0016	0.0035	0.4527	2.2091
Brain	0.0017	0.0010	1.7408	0.5745
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0046	0.0000	undef	0.0000
Heart	0.0112	0.0275	0.4061	2.4624
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0019	0.0074	0.2631	3.8007
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0086	0.0000	undef	0.0000
Kidney	0.0022	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0019	0.0000	undef	0.0000
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0044	0.0092	0.4819	2.0750
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0013			
Penis	0.0080			
Seminal vesicle	0.0070			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0242
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0191
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0065
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

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Electronic Northern for Seq. ID: 168

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0132	0.0000	undef 0.0000
Large intestine	0.0057	0.0000	undef 0.0000
Small intestine	0.0000	0.0107	0.0000 undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0016	0.0000	undef 0.0000
Brain	0.0006	0.0030	0.1934 5.1701
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0039	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0034	0.0037	0.9278 1.0778
Pancreas	0.0045	0.0000	undef 0.0000
Prostate	0.0000	0.0000	undef undef
T lymphoma	0.0047	0.0039	1.2059 0.8293
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0044	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0013		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

REBUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0051
Ovary_t	0.0000
Endocrine tissue	0.0023
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

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Electronic Northern for Seq. ID: 169

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0039	0.0023	1.6595	0.6026
Breast	0.0106	0.0028	3.7573	0.2662
Large intestine	0.0096	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0032	0.0018	1.8107	0.5523
Brain	0.0012	0.0030	0.3868	2.5851
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0046	0.0000	undef	0.0000
Heart	0.0020	0.0000	undef	0.0000
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0039	0.0000	undef	0.0000
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0069	0.0037	1.8555	0.5389
Kidney	0.0112	0.0048	2.3212	0.4308
Pancreas	0.0033	0.0000	undef	0.0000
Prostate	0.0009	0.0000	undef	0.0000
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0044	0.0046	0.9638	1.0375
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0013			
Penis	0.0027			
Seminal vesicle	0.0000			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0490
Fetal	0.0197
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0020
Ovary uterus	0.0000
Prostate n	0.0045
Sensory organs	0.0121
White blood cells	0.0000
	0.0000

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Electronic Northern for Seq. ID: 170

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0117	0.0141	0.8297 1.2052
Breast	0.0194	0.0056	3.4442 0.2903
Large intestine	0.0057	0.0000	undef 0.0000
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0000	0.0024	0.0000 undef
Endocrine tissue	0.0032	0.0018	1.8107 0.5523
Brain	0.0069	0.0140	0.4974 2.0106
Skin	0.0367	0.0000	undef 0.0000
Hepatic	0.0046	0.0000	undef 0.0000
Heart	0.0101	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef 0.0000
Lung	0.0049	0.0055	0.8770 1.1402
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0103	0.0000	undef undef
Kidney	0.0134	0.0048	2.7855 0.3590
Pancreas	0.0017	0.0055	0.2992 3.3427
Prostate	0.0028	0.0013	2.1706 0.4607
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0030	0.0000	undef 0.0000
White blood cells	0.0199	0.0000	undef 0.0000
Hematopoietic	0.0040	0.0000	undef 0.0000
Penis	0.0000		
Seminal vesicle	0.0141		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0065
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0050
Ovary Uterus	0.0000
Prostate n	0.0023
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 171

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0250	0.0000	undef	0.0000
Bladder	0.0546	0.0188	2.9041	0.3443
Breast	0.0387	0.0056	6.8883	0.1452
Large intestine	0.0287	0.0000	undef	0.0000
Small intestine	0.0302	0.0107	2.8342	0.3528
Ovary	0.0237	0.0024	9.9547	0.1005
Endocrine tissue	0.0112	0.0106	1.0563	0.9467
Brain	0.0093	0.0060	1.5474	0.6463
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0046	0.0063	0.7324	1.3653
Heart	0.0304	0.0000	undef	0.0000
Testicles	0.0161	0.0000	undef	0.0000
Lung	0.0175	0.0092	1.8944	0.5279
Stomach-esophagus	0.0145	0.0064	2.2671	0.4411
Muscle-skeleton	0.0188	0.0074	2.5514	0.3919
Kidney	0.0134	0.0048	2.7855	0.3590
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0254	0.0221	1.1491	0.8702
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0414	0.0184	2.2490	0.4446
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0160			
Penis	0.0724			
Seminal vesicle	0.0352			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0197
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0036
Lung	0.0181
Adrenal gland	0.0254
Kidney	0.0309
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0952
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0127
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0040
Ovary Uterus	0.0000
Prostate n	0.0203
Sensory organs	0.0243
White blood cells	0.0000
	0.0000

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Electronic Northern for Seq. ID: 172

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0039	0.0023	1.6595 0.6026
Breast	0.0176	0.0042	4.1747 0.2395
Large intestine	0.0038	0.0028	1.3456 0.7432
Small intestine	0.0137	0.0107	1.2883 0.7762
Ovary	0.0000	0.0048	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0006	0.0090	0.0645 15.5103
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0081	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0029	0.0037	0.7893 1.2669
Muscle-skeleton	0.0072	0.0192	0.3778 2.6466
Kidney	0.0154	0.0037	4.1750 0.2395
Pancreas	0.0022	0.0048	0.4642 2.1540
Prostate	0.0000	0.0000	undef undef
T lymphoma	0.0132	0.0052	2.5323 0.3949
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0030	0.0322	0.0918 10.8939
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Seminal vesicle	0.0080		
Sensory organs	0.0141		

0.0118
FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0181
Adrenal gland	0.0254
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0020
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

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Electronic Northern for Seq. ID: 173

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0050	0.0000	undef	0.0000
Bladder	0.0000	0.0047	0.0000	undef
Breast	0.0053	0.0014	3.7573	0.2662
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0089	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0089	0.0000	undef
Brain	0.0006	0.0030	0.1934	5.1701
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0088	0.0000	undef	0.0000
Muscle-skeleton	0.0217	0.0000	undef	0.0000
Kidney	0.0034	0.0074	0.4639	2.1557
Pancreas	0.0022	0.0000	undef	0.0000
Prostate	0.0017	0.0055	0.2992	3.3427
T lymphoma	0.0047	0.0039	1.2059	0.8293
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0030	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Penis	0.0027	0.0000	undef	undef
Seminal vesicle	0.0054			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0063
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0203
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0030
Ovary uterus	0.0000
Prostate n	0.0090
Sensory organs	0.0061
White blood cells	0.0000

0.0000

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Electronic Northern for Seq. ID: 174

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0100	0.0136	0.7358	1.3590
Bladder	0.0078	0.0070	1.1063	0.9039
Breast	0.0114	0.0028	4.0704	0.2457
Large intestine	0.0077	0.0057	1.3456	0.7432
Small intestine	0.0082	0.0213	0.3865	2.5875
Ovary	0.0000	0.0072	0.0000	undef
Endocrine tissue	0.0032	0.0000	undef	0.0000
Brain	0.0017	0.0090	0.1934	5.1701
Skin	0.0073	0.0394	0.1862	5.3697
Hepatic	0.0093	0.0063	1.4649	0.6826
Heart	0.0010	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0107	0.0092	1.1577	0.8638
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0377	0.0037	10.2055	0.0980
Kidney	0.0000	0.0096	0.0000	undef
Pancreas	0.0000	0.0110	0.0000	undef
Prostate	0.0028	0.0026	1.0853	0.9214
T lymphoma	0.0051	0.0075	0.6762	1.4788
Uterus	0.0030	0.0046	0.6426	1.5563
White blood cells	0.0164	0.0304	0.5410	1.8483
Hematopoietic	0.0094			
Penis	0.0027			
Seminal vesicle	0.0000			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
0.0000 % frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0152
Ovary_t	0.0735
Endocrine tissue	0.0151
Fetal	0.0366
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0225
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

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	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0312	0.0047	6.6380 0.1506
Breast	0.0158	0.0056	2.8179 0.3549
Large intestine	0.0038	0.0000	undef 0.0000
Small intestine	0.0082	0.0213	0.3865 2.5875
Ovary	0.0059	0.0024	2.4887 0.4018
Endocrine tissue	0.0177	0.1277	0.1383 7.2297
Brain	0.0220	0.0100	2.2050 0.4535
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0244	0.0275	0.8861 1.1286
Lung	0.0040	0.0000	undef 0.0000
Stomach-esophagus	0.0078	0.0037	2.1049 0.4751
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0120	0.0000	undef 0.0000
Pancreas	0.0000	0.0145	0.0000 undef
Prostate	0.0000	0.0110	0.0000 undef
T lymphoma	0.0075	0.0078	0.9647 1.0366
Uterus	0.0025	0.0000	undef 0.0000
White blood cells	0.0103	0.0046	2.2490 0.4446
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0013		
Seminal vesicle	0.0375		
Sensory organs	0.0141		
	0.0353		

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0254
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
0.0068 % frequency

Breast	0.0068
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0490
Fetal	0.0035
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0161
Kidney_t	0.0000
Ovary uterus	0.0045
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 176

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0078	0.0047	1.6595	0.6026
Breast	0.0202	0.0028	7.2014	0.1389
Large intestine	0.0057	0.0142	0.4037	2.4773
Small intestine	0.0110	0.0000	undef	0.0000
Ovary	0.0030	0.0072	0.4148	2.4109
Endocrine tissue	0.0064	0.0035	1.8107	0.5523
Brain	0.0058	0.0020	2.9013	0.3447
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0081	0.0000	undef	0.0000
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0068	0.0055	1.2278	0.8144
Stomach-esophagus	0.0000	0.0064	0.0000	undef
Muscle-skeleton	0.0017	0.0037	0.4639	2.1557
Kidney	0.0022	0.0048	0.4642	2.1540
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0028	0.0026	1.0853	0.9214
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0030	0.0000	undef	0.0000
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0027			
Penis	0.0054			
Seminal vesicle	0.0000			
Sensory organs	0.0235			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0020
Kidney_t	0.0000
Ovary uterus	0.0135
Prostate_n	0.0061
Sensory organs	0.0155
White blood cells	0.0000

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Electronic Northern for Seq. ID: 177

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0000	undef 0.0000
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0079	0.0014	5.6359 0.1774
Large intestine	0.0096	0.0000	undef 0.0000
Small intestine	0.0000	0.0107	0.0000 undef
Ovary	0.0000	0.0024	0.0000 undef
Endocrine tissue	0.0016	0.0089	0.1811 5.5227
Brain	0.0023	0.0050	0.4642 2.1542
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0127	0.0000 undef
Heart	0.0030	0.0137	0.2215 4.5144
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0019	0.0018	1.0524 0.9502
Stomach-esophagus	0.0000	0.0128	0.0000 undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0045	0.0000	undef 0.0000
Pancreas	0.0033	0.0000	undef 0.0000
Prostate	0.0066	0.0026	2.5323 0.3949
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0015	0.0046	0.3213 3.1125
White blood cells	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0040		
Penis	0.0080		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0040
Ovary uterus	0.0000
Prostate n	0.0090
Sensory organs	0.0061
White blood cells	0.0000

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Electronic Northern for Seq. ID: 178

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0078	0.0258	0.3017	3.3143
Breast	0.0070	0.0042	1.6699	0.5988
Large intestine	0.0172	0.0114	1.5138	0.6606
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0167	0.0000	undef
Endocrine tissue	0.0080	0.0018	4.5268	0.2209
Brain	0.0041	0.0080	0.5077	1.9696
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0046	0.0190	0.2441	4.0959
Heart	0.0112	0.0137	0.8122	1.2312
Testicles	0.0000	0.0000	undef	undef
Lung	0.0214	0.0240	0.8905	1.1229
Stomach-esophagus	0.0362	0.0192	1.8892	0.5293
Muscle-skeleton	0.0137	0.0074	1.8555	0.5389
Kidney	0.0000	0.0048	0.0000	undef
Pancreas	0.0116	0.0166	0.6980	1.4326
Prostate	0.0104	0.0182	0.5685	1.7591
T lymphoma	0.0051	0.0000	undef	0.0000
Uterus	0.0044	0.0046	0.9638	1.0375
White blood cells	0.0055	0.0000	undef	0.0000
Hematopoietic	0.0053			
Penis	0.0107			
Seminal vesicle	0.0000			
Sensory organs	0.0235			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0108
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0242
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0081
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0293
Lungs_t	0.0000
Nerves	0.0030
Kidney_t	0.0000
Ovary uterus	0.0045
Prostate_n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

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2.2. Fisher Test

In order to decide whether a partial sequence S of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to S . If the null hypothesis can be rejected with high enough certainty, the gene belonging to S is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic lengthening of the partial sequence

Automatic lengthening of partial sequence S is completed in three steps:

1. Determination of all sequences homologous to S from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence C from the assembled sequences.

The consensus sequence C will generally be longer than initial sequence S . Its electronic Northern Blot will

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accordingly deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i : iteration index) obtained in each case until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from breast tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORFs) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

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Mapping of nucleic acid sequences on the human genome

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the gap between genome mapping and genome sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence mapping by electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic sequences that correspond to the differential cDNAs were isolated from commercial BAC libraries. BAC libraries of the Genome Systems Company, St. Louis, MO, which were produced from human lymphocytes, were used (<http://www.genomesystems.com>) and those of the Research Genetics Company, which were described as follows, were used: Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797; <http://www.tree.caltech.edu/>. From these libraries, the BAC clones with the procedure of "down-to-the-well" were isolated. In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is combined in various groups (pools). This takes place in such a way that after the execution of a gene-specific PCR in the various pools, a definite clone assignment is possible. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries of genome systems used were CITB B and CITB C. Clones from the library of Research Genetics are underlined.

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Normal Breast

Seq. ID No.	Identified BACs				
4	174/F/16				
12	388/D/5	393/M/24	494/B/3	502/B/23	
13	<u>203/A/1</u>	<u>233/B/22</u>	392/L/10	<u>311/J/7</u>	
15	<u>248/C/14</u>	<u>266/E/16</u>	528/D/3	<u>266/E/17</u>	<u>506/P/12</u>
19	<u>113/G/13</u>	191/B/19	<u>202/O/3</u>	<u>250/O/19</u>	
21	137/H/19	231/I/10			
22	165/N/5	208/D/7			
26	6/L/15	11/I/17	117/E/15		
28	<u>501/L/21</u>	<u>367/D/6</u>			
31	<u>369/H/21</u>	<u>429/I/13</u>			
34	<u>108/M/13</u>				
37	289/C/11				
42	59/A/20				
43	<u>325/J/11</u>	<u>448/O/2</u>	<u>563/F/18</u>		
57	4/G/9				
58	229/O/21	233/F/12			
59	97/P/23	109/A/1	125/H/9		
60	<u>503/P/21</u>				
61	3/P/21	188/B/9			
63	176/A/22				
69	425/E/10				
71	178/I/19	242/B/6	242/B/11		

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TABLE I

Col. 1 - Ser. No.
 Col. 2 - Expression
 Col. 3 - Function
 Col. 4 - Modules
 Col. 5 - Chromosomal localization
 Col. 6 - Next marker
 Col. 7 - EST length (bp)
 Col. 8 - Length of the applied sequence (bp)

[Key:]

unbekannt = unknown

zwischen...und = between...and

Domäne = domain

"PH"-Domäne und "Spectrin"-Domäne = "PH" domain and "spectrin" domain

"crystallin"-Domäne und "HSP20"-Domäne = "crystalline" domain and "HSP20" domain

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TABLE I

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"crystallin"-Domäne und "HSP20"-Domäne = "crystalline" domain and "HSP20" domain

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TABLE I

Ser. No.	Expression	Function
1	Elevated in normal breast tissue	A new human pre-mRNA splice factor, which is part of a gene family with a TPR (tetratricopeptide repeats) motif.
2	Elevated in normal breast tissue	Unknown
3	Elevated in normal breast tissue	The human homolog of perilipin A from the rat.
4	Elevated in normal breast tissue	Unknown
5	Elevated in normal breast tissue	Unknown
10	Elevated in normal breast tissue	A human ortholog of fsp-27 (fat-specific protein 27) of the mouse.
11	Elevated in normal breast tissue	Unknown
12	Elevated in normal breast tissue	Unknown

[Key:]

unbekannt = unknown

zwischen...und = between...and

lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
1	im normalen Brustgewebe erhöht	Ein neuer humaner Prä-mRNA Spleiß-Faktor, der zur einer Genfamilie mit TPR (Tetratricopeptid repeats)-Motiv gehört.	"TPR"-Region	unbekannt	unbekannt	205	2031
2	im normalen Brustgewebe erhöht	unbekannt		3q29	zwischen D3S1265 und D3S1311	248	1081
3	im normalen Brustgewebe erhöht	Das humane Homolog des Perilipin A aus Ratte.		15q26.1-qter	SHGC-6068; zwischen WI-7918 und SHGC-14718	247	1318
4	im normalen Brustgewebe erhöht	unbekannt		Xq24	SHGC-14021 alias DXS9764	256	731
5	im normalen Brustgewebe erhöht	unbekannt		15q26.1-qter	D15S120-15qter	237	2719
10	im normalen Brustgewebe erhöht	Ein humanes Ortholog des fsp-27 (Fett-spezifisches Protein 27) der Maus.		3p24.3-p25.1	zwischen D3S1597 und D3S1263	310	1107
11	im normalen Brustgewebe erhöht	unbekannt		17q22-q23.2	SHGC-32689; zwischen D17S787 und D17S792	239	1062
12	im normalen Brustgewebe erhöht	unbekannt		2q34	SHGC-3316; zwischen D2S315 und D2S2237	241	1471

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[Key:]
Domäne = domain
unbekannt = unknown
zwischen...und = between...and
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lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
13	im normalen Brustgewebe erhöht	Das humane LOT1 (Lost On Transformation 1).	"ZINC_FINGER_C2H2_2_2"-Domäne	6q23.3-q24.3	zwischen D6S308 und D6S978	214	2738
14	im normalen Brustgewebe erhöht	Das humane SGN3 (die Untereinheit 3 eines JAB1 enthaltenden Signalosoms).	"PCI_DOMAIN"	17p12-q11.2	sts-W80395; zwischen D17S922 und D17S798	225	1710
15	im normalen Brustgewebe erhöht	Ein neues Zinkfinger-Protein des LIM-Typs.	"LIM"-Domäne	4p14	SHGC4-435; zwischen SHGC4-259 und SHGC-33782	228	3159
16	im normalen Brustgewebe erhöht	Der humane nukleärer Faktor I-B2 (NFIB2).		unbekannt	unbekannt	249	1680
18	im normalen Brustgewebe erhöht	Das humane Dermato pontin.		1q12-q23	unbekannt	188	1722
19	im normalen Brustgewebe erhöht	unbekannt		1p22.1-p22.2	SHGC-34523	287	1612
21	im normalen Brustgewebe erhöht	unbekannt		11q14.1	SHGC-32865; zwischen SHGC-3911 und SHGC-36303	248	1304

Ser. No.	Expression	Function
22	Elevated in normal breast tissue	This sequence is related to heavy chain H3 of the human inter-alpha-trypsin inhibitor. The latter possibly plays a role in the stabilization of the extracellular matrix.
23	Elevated in normal breast tissue	Unknown
24	Elevated in normal breast tissue	Unknown
25	Elevated in normal breast tissue	Unknown
26	Elevated in normal breast tissue	The pi-subunit of the human GABA-A receptor.
28	Elevated in normal breast tissue	This sequence is possibly the ortholog of the neural membrane protein 35 (NMP35) of the rat.

[Key:]

Domäne = domain

zwischen...und = between...and

lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
22	im normalen Brustgewebe erhöht	Diese Sequenz ist verwandt mit der schweren Kette H3 des humanen Inter-alpha-Trypsin Inhibitors. Dieser spielt möglicherweise eine Rolle bei der Stabilisierung der extrazellulären Matrix.		10p15.1-p15.3	SHGC-16603; zwischen SHGC-16603 und SHGC-33903	288	1533
23	im normalen Brustgewebe erhöht	unbekannt		11q14.2-q14.3	zwischen D11S1354 und D11S931	204	1304
24	im normalen Brustgewebe erhöht	unbekannt		10p15.1-p15.3	zwischen D10S591 und D10S189	291	2403
25	im normalen Brustgewebe erhöht	unbekannt		2q35	AFM249wg9; zwischen CHLC.GATA29E02 und WI-7744	286	2517
26	im normalen Brustgewebe erhöht	Die pi-Untereinheit des humanen GABA-A Rezeptors.	"neur_cha n"-Domäne	5q34	AFM304xd5; zwischen AFM080xh11 und SHGC-5539	268	1668
28	im normalen Brustgewebe erhöht	Diese Sequenz ist möglicherweise das Ortholog des Neuralen Membran Protein 35 (NMP35) der Ratte.	"UPF0005"-Domäne	2q35	SHGC-35278; zwischen D2S164 und D2S163	244	1768

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Ser. No.	Expression	Function
29	Elevated in normal breast tissue	The human β -spectrin.
30	Elevated in normal breast tissue	Unknown
31	Elevated in normal breast tissue	This sequence probably represents the human ortholog of the "SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2)" of the hamster.
32	Elevated in normal breast tissue	The human protein kinase A anchor-protein; it binds the regulatory subunit (RII) of the protein-kinase A.
33	Elevated in normal breast tissue	The human Mi-2 autoantigen, in this connection it is presumably a helicase, which activates the transcription.
34	Elevated in normal breast tissue	Unknown
35	Elevated in normal breast tissue	The human "obese protein" (ob).

lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
29	im normalen Brustgewebe erhöht	Das humane β -Spectrin.	"PH"-Domäne und "Spectrin"-Domäne	2p16.1-16.3	zwischen D2S123 und D2S378	247	3479
30	im normalen Brustgewebe erhöht	unbekannt		7p21.2-p21.3	SHGC-35668; zwischen D7S714 und D7S2564	88	933
31	im normalen Brustgewebe erhöht	Diese Sequenz stellt wahrscheinlich das humane Ortholog des "SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2)" des Hamsters dar.	"LIM"-Domäne	12p11.21-q13.11	zwischen D12S1648 und D12S1620	269	2783
32	im normalen Brustgewebe erhöht	Das humane Protein Kinase A Anker-Protein; es bindet die regulatorische Untereinheit (RII) der Protein-Kinase A.	"KH"-Domäne und "TUDOR"-Domäne	17q22	zwischen D17S790 und D17S794	265	3411
33	im normalen Brustgewebe erhöht	Das humane Mi-2 Autoantigen, es handelt sich hierbei vermutlich um eine Helicase, die die Transkription aktiviert.		12p12.3-p13.33	zwischen D12S93 und D12S77	244	1393
34	im normalen Brustgewebe erhöht	unbekannt		10q25.1	SHGC-14061; zwischen ATC3 und AFMa273ye1	258	1236
35	im normalen Brustgewebe erhöht	Das humane "obese protein" (ob).		7q31.3	zwischen D7S686 und D7S530	237	749

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Ser. No.	Expression	Function
36	Elevated in normal breast tissue	The human Duffy-antigen (DARC gene).
37	Elevated in normal breast tissue	This protein has an approximately 50% amino acid identity with S3-12, a plasma membrane-associated protein, which is expressed during the fat cell differentiation.
38	Elevated in normal breast tissue	The human semaphorin E; it possibly mediates cellular resistance against cis-platinum (CDDP), a substance that is frequently used in chemotherapy.
39	Elevated in normal breast tissue	The human alpha-B-crystalline gene, originally cloned as a lens-specific gene, seems to be regulated by progesterone and estrogen in the endometrium. The expression correlates with the non-proliferative phase of the menstrual cycle.
40	Elevated in normal breast tissue	The human extracellular protein S1-5.
41	Elevated in normal breast tissue	The human lipoprotein-lipase.

I fd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
36	im normalen Brustgewebe erhöht	Das humane Duffy-Antigen (DARC-Gen).		1q22	zwischen D1S484 und D1S426	271	1251
37	im normalen Brustgewebe erhöht	Dieses Protein hat eine ca. 50%ige Aminosäure-Identität zu S3-12, einem Plasma Membran-assoziiertem Protein, das während der Fettzellen-Differenzierung exprimiert wird.		unbekannt	unbekannt	199	3283
38	im normalen Brustgewebe erhöht	Das humane Semaphorin E; es vermittelt möglicherweise zelluläre Resistenz gegen cis-Platinum (CDDP), einer in der Chemotherapie häufig verwendeten Substanz.		7q11.23-q21.13	stSG30323; zwischen D7S660 und D7S524	240	2720
39	im normalen Brustgewebe erhöht	Das humane alpha-B-Crystallin-Gen, ursprüngl. als linsen-spezifisches Gen kloniert, scheint im Endometrium durch Progesteron und Östrogen reguliert zu werden. Die Expression korreliert mit der Nicht-proliferativen Phase des Menstruationszyklus.	"crystallin"-Domäne und "HSP20"-Domäne	11q23.1-q23.2	zwischen D11S1893 und D11S938	247	1036
40	im normalen Brustgewebe erhöht	Das humane extrazelluläres Protein S1-5.	"EGF_CA"-Domäne	2p11.1-12	zwischen D2S2371 und D2S388	265	2659
41	im normalen Brustgewebe erhöht	Die humane Lipoprotein-Lipase.	"Lipase"-Domäne	8p22-p23.1	zwischen D8S261 und D8S258	252	2939

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Ser. No.	Expression	Function
42	Elevated in normal breast tissue	The human sFRP ("secreted frizzled-related protein") plays a role in programmed cell death (apoptosis)
43	Elevated in normal breast tissue	Unknown
45	Elevated in normal breast tissue	This sequence is probably the human ortholog of a fat cell-specific gene of the mouse.
47	Elevated in normal breast tissue	The human placenta "copper monoamine oxidase."
48	Elevated in normal breast tissue	Unknown
49	Elevated in normal breast tissue	The human "ras-like protein."
50	Elevated in normal breast tissue	Unknown
51	Elevated in normal breast tissue	Unknown
53	Elevated in normal breast tissue	The YAP (Yes-associated protein); it binds to SH3-domains.

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
42	im normalen Brustgewebe erhöht	Das humane sFRP ("secreted frizzled-related protein") spielt eine Rolle beim programmierten Zelltod (Apoptosis).		8p11.21-p12	zwischen D8S1791 und D8S268	404	3670
43	im normalen Brustgewebe erhöht	unbekannt		10q23.32-q25.1	WI-14063	259	1025
45	im normalen Brustgewebe erhöht	Diese Sequenz ist wahrscheinlich das humane Ortholog eines Fettzellen-spezifischen Gens der Maus.		unbekannt	unbekannt	328	538
47	im normalen Brustgewebe erhöht	Die humane Plazenta "copper monamine oxidase".		17q12	SHGC-3147	256	360
48	im normalen Brustgewebe erhöht	unbekannt	"HSP20"-Domäne	1p36.13-p36.23	zwischen D1S434 und D1S507	157	2192
49	im normalen Brustgewebe erhöht	Das humane "ras-like protein".	"ras"-Domäne	2p16.3-p21	zwischen D2S391 und D2S123	305	2952
50	im normalen Brustgewebe erhöht	unbekannt		7p12.1-p12.3	zwischen D7S506 und D7S659	188	615
51	im normalen Brustgewebe erhöht	unbekannt		11q12.1-q13.1	SHGC-35409; WI-7266 - D11S2006	290	1488
53	im normalen Brustgewebe erhöht	Das YAP (Yes-associated protein); es bindet an SH3-Domänen.		11q21.1-q22.3	D11S1339	289	2262

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Ser. No.	Expression	Function
54	Elevated in normal breast tissue	The human B4-2 protein.
56	Elevated in normal breast tissue	The human "long-chain acyl-CoA synthetase."
57	Elevated in normal breast tissue	The "prepro-melanine-concentrating hormone."
58	Elevated in normal breast tissue	Unknown
59	Elevated in normal breast tissue	A possible new member of the human tob-gene family.
60	Elevated in normal breast tissue	Unknown
61	Elevated in normal breast tissue	The human ortholog to the kryn gene of the mouse.
62	Elevated in normal breast tissue	Unknown

[Key:]

Domäne = domain

zwischen...und = between...and

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
54	im normalen Brustgewebe erhöht	Das humane B4-2 Protein.		6q16.2	SHGC-31472	306	1301
56	im normalen Brustgewebe erhöht	Die humane "Lange Ketten Acyl-CoA Synthetase".		4q33-q35.2	zwischen D4S408 und D4S426	269	1265
57	im normalen Brustgewebe erhöht	Das "Prepro-Melanin-konzentrierende Hormon (prepro-melanin-concentrating hormone)".		12q22	AFM263ZD1; zwischen SHGC-15767 und SHGC-9350	247	274
58	im normalen Brustgewebe erhöht	unbekannt		2q22.3-2q23.2	SHGC-36777	270	2073
59	im normalen Brustgewebe erhöht	Ein mögliches neues Mitglied der humanen tob-Genfamilie.		21q11.1-q21.1	SHGC-11705; zwischen D21S1886 und D21S1256	205	850
60	im normalen Brustgewebe erhöht	unbekannt		1q22	SHGC-36663; zwischen SGC32839 und D1S1576	229	2091
61	im normalen Brustgewebe erhöht	Das humane Ortholog zum Kryn-Gen der Maus.	"SH3"-Domäne	4q31.3	SHGC-31182	225	2952
62	im normalen Brustgewebe erhöht	unbekannt		11p15.3	AFM166zel; zwischen SHGC-5993 und SHGC-13819	223	2313

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Ser. No.	Expression	Function
63	Elevated in normal breast tissue	Unknown
64	Elevated in normal breast tissue	The human ortholog to UMP-CMP kinase of the pig.
65	Elevated in normal breast tissue	Unknown
66	Elevated in normal breast tissue	The human cAMP phosphodiesterase.
67	Elevated in normal breast tissue	The human antigen CD 36.
68	Elevated in normal breast tissue	Presumably a human ortholog of the yeast <i>S. pombe</i> sad1 + gene.
69	Elevated in normal breast tissue	Unknown
71	Elevated in normal breast tissue	A new human protein, which contains an SH3-domain. These proteins are mediators of the intercellular cell communication.

[Key:]

Domäne = domain

zwischen...und = between...and

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
63	im normalen Brustgewebe erhöht	unbekannt		2q24.1-q24.3	SHGC-1305; zwischen CHLC.GATA22H09 und WI-7620	192	1650
64	im normalen Brustgewebe erhöht	Das humane Ortholog zur UMP-CMP Kinase des Schweins.	"Adenylate-kinase"	1p32.3-p36.12	SHGC-36697; zwischen D1S2843 und D1S417	223	2851
65	im normalen Brustgewebe erhöht	unbekannt		4p15.1	WI-15951; zwischen D4S1043 und SHGC-16179	221	1071
66	im normalen Brustgewebe erhöht	Die humane cAMP Phosphodiesterase.	"PDEase"	8q13.1	CHLC.GATA86D08; zwischen SHGC-9281 und AFMa084wc5	199	2375
67	im normalen Brustgewebe erhöht	Das humane Antigen CD 36.	"CD36"-Domäne	7q11.23	sWSS1455	221	1823
68	im normalen Brustgewebe erhöht	Vermutlich ein humanes Ortholog des Hefe <i>S. pombe</i> sad1+ Gens.		7p22.3	SHGC-34866; zwischen SHGC-10715 und SHGC-32510	248	2403
69	im normalen Brustgewebe erhöht	unbekannt		5p15.33	zwischen D5S477 und D5S426	230	1246
71	im normalen Brustgewebe erhöht	Ein neues humanes Protein, das eine SH3-Domäne enthält. Diese Proteine sind Mediatoren der interzellulären Zellkommunikation.		8p21.3	SHGC-30970	263	1950

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Ser. No.	Expression	Function
72	Elevated in normal breast tissue	A new human gene, which possibly represents a transcription factor; a certain sequence identity with the DNA-binding protein CROC-1A exists on the nucleic acid plane.
74	Elevated in normal breast tissue	Presumably the human ortholog of the mouse Sox-18. The Sox proteins represent an important group of transcription factors that control development processes. Sox-genes have a so-called HMG-box ("high mobility group"). Mouse-Sox 18 is related to Sry ("testis-determining factor") of the human.
76	Elevated in normal breast tissue	Unknown

[Key:]

unbekannt = unknown

zwischen...und = between...and

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
72	im normalen Brustgewebe erhöht	Ein neues humanes Gen, das möglicherweise einen Transkriptionsfaktor darstellt; auf Nukleinsäure-Ebene besteht eine gewisse Sequenzidentität zu dem DNA-bindenden Protein CROC-1A.		7q21.11-q22.1	R06442; zwischen D7S524 und D7S657	240	814
74	im normalen Brustgewebe erhöht	Vermutlich das humane Ortholog des Maus Sox-18. Die Sox-Proteine stellen eine wichtige Gruppe von Transkriptionsfaktoren dar, die Entwicklungsprozesse steuern. Sox-Gene weisen eine sog. HMG-Box ("high mobility group") auf. Maus-Sox 18 ist verwandt mit Sry ("testis-determining factor") des Menschen.		unbekannt	unbekannt	264	747
76	im normalen Brustgewebe erhöht	unbekannt		17p13.3-q25.3	AFM163yg1	296	2419

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Ser. No.	Expression	Module
161	Elevated in normal breast tissue	Lengthening to Seq. ID No. 1
162	Elevated in normal breast tissue	Lengthening to Seq. ID No. 4
163	Elevated in normal breast tissue	Lengthening to Seq. ID No. 10
164	Elevated in normal breast tissue	Lengthening to Seq. ID No. 11
165	Elevated in normal breast tissue	Lengthening to Seq. ID No. 12

[Key:]

Domäne = domain

unbekannt = unknown

zwischen...und = between...and

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
161	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.1	"RGS"-Domäne; "ATP-synt_B"-Domäne; "TPR_Region TPR repeat"; "NLS_BP Bipartite nuclear localization signal"	unbekannt	unbekannt	205	3096
162	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.4	"CNH"-Domäne; "NLS_BP Bipartite nuclear localization signal"	Xq24	SHGC-14021 alias DXS9764	256	1987
163	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.10		3p24.3-p25.1	zwischen D3S1597 und D3S1263	310	1107
164	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.11	"TK"-Domäne	17q22-q23.2	SHGC-32689; zwischen D17S787 und D17S792	239	1062
165	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.12	"Polyoma_coat2"-Domäne	2q34	SHGC-3316; zwischen D2S315 und D2S2237	241	2770

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[Key:]
Domäne = domain
zwischen...und = between...and
```

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
166	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.15	LIM; Ran_BP1; NLS_BP Bipartite nuclear localization signal	4p14	SHGC4-435; zwischen SHGC4-259 und SHGC-33782	228	4242
167	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.19	"UPF0024"-Domäne	1p22.1-p22.2	SHGC-34523	287	2640
168	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.22		10p15.1-p15.3	SHGC-16603; zwischen SHGC-16603 und SHGC-33903	288	1558
169	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.23		11q14.2-q14.3	zwischen D11S1354 und D11S931	204	1388
170	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.24	"ribonuclease_T 2"-Domäne	10p15.1-p15.3	zwischen D10S591 und D10S189	291	2416
171	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.25	"TK"-Domäne	2q35	AFM249wg9; zwischen CHLC.GATA29E02 und WI-7744	286	2720
172	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.38	"ig"-Domäne	7q11.23-q21.13	stSG30323; zwischen D7S660 und D7S524	240	2987
173	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.50		7p12.1-p12.3	zwischen D7S506 und D7S659	188	892

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[Key:]
Domäne = domain
zwischen...und = between...and
```

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
174	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.51	"NLS_BP Bipartite nuclear localization signal"	11q12.1-q13.1	SHGC-35409; zwischen WI-7266 und D11S2006	290	1679
175	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.60	"NLS_BP Bipartite nuclear localization signal"	1q22	SHGC-36663; zwischen SGC32839 und D1S1576	229	2411
176	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.61	"SH3"-Domäne; "IL-6"-Domäne; "toxin 2"-Domäne	4q31.3	SHGC-31182	225	3450
177	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.72		7q21.11-q22.1	R06442; zwischen D7S524 und D7S657	240	874
178	im normalen Brustgewebe erhöht	unbekannt	"PH"-Domäne	9q34.11-q34.12	stSG3880; zwischen D9S1821 und D9S159	242	3265

TABLE II

DNA Sequences
Seq. ID. No.

Peptide Sequences
Seq. ID. No.

1	77
2	78
	79
	80
	81
3	82
4	83
5	84
10	85
11	87
12	88
13	89
14	90
15	91
18	92
19	93
21	95
22	96
23	97
24	98
	99
25	100
	101
	102
	103
28	104

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DNA Sequences
Seq. ID. No.

Peptide Sequences
Seq. ID. No.

30

105

106

107

31

108

34

112

37

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42

114

43

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116

117

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119

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149

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151

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DNA Sequences
Seq. ID. No.**Peptide Sequences**
Seq. ID. No.

161

162

163

164

165

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171

172

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The inventive nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID No. 178 of the determined candidate genes and the determined amino acid sequences Seq. ID No. 77 to Seq. ID No. 160 and Seq. ID No. 179 to Seq. ID No. 209 are described in the following sequence protocol.

Sequence Protocol

(1) GENERAL INFORMATION:

(i) APPLICANT

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1672
- (H) FAX: (030)-8413 1671

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Breast Tissue

(iii) Number of sequences: 183

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

000260" 69594960

(2) INFORMATION ON SEQ ID NO. 1:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2031 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATTGCATCAG	CCCGCCTGGA	AGAAGTCACT	GGGAAGCTAC	AAGTAGCTCG	GAACCTTATC	60
ATGAGGGGGA	CGGAGATGTG	CCCCAAGAGT	GAAGATGTCT	GGCTGGAAGC	AGCCAGGTTG	120
CAGCCTGGGG	ACACAGCCAA	GGCCGTGGTA	GCCCAAGCTG	TCCGTCATCT	CCCACAGTCT	180
GTCAGGATTT	ACATCAGAGC	CGCAGAGCTG	GAAACGGACA	TTCGTGCAAA	GAAGCGGGTT	240
CTTCGGAAAAG	CCCTCGAGCA	TGTTCCAAAC	TCGGTTCGCT	TGTGGAAAGC	AGCCGTTGAG	300
CTGGAAGAAC	CTGAAGATGC	TAGAATCATG	CTGAGCCGAG	CTGTGGAGTG	CTGCCCCACC	360
AGCGTGGAGC	TCTGGCTTGC	TCTGGCAAGG	CTGGAGACCT	ATGAAAATGC	CCGCAAGGTC	420
TTGAACAAGG	CGCGGGAGAA	CATTCTTACA	GACCGACATA	TCTGGATCAC	GGCTGCTAAG	480
CTGGAGGAAG	CCAATGGGAA	CACGCAGATG	GTGGAGAAGA	TCATCGACCG	AGCCATCACC	540
TCGCTGCGGG	CCAACGGTGT	GGAGATCAAC	CGTGAGCAGT	GGATCCAGGA	TGCCGAGGAA	600
TGTGACAGGG	CTGGGAGTGT	GGCCACCTGC	CAGGCCGTCA	TGCGTGCCGT	GATTGGGATT	660
GGGATTGAGG	AGGAAGATCG	GAAGCATACC	TGGATGGAGG	ATGCTGACAG	TTGTGTAGCC	720
CACAATGCCC	TGGAGTGTGC	ACGAGCCATC	TACGCCTACG	CCCTGCAGGT	GTTCCCCAGC	780
AAGAAGAGTG	TGTGGCTGCG	CGCCGCGTAC	TTGAGAAAGA	ACCATGGCAC	TCGGGAGTCC	840
CTGGAAGCAC	TCCTGCAGAG	GGCTGTGGCC	CACTGCCCCA	AAGCAGAGGT	GCTGTGGCTC	900
ATGGGCGCCA	ATGTTCAAGT	GCTGGCAGGG	GATGTGCCTG	CAGCAAGGAG	CATCCTGGCC	960
CTGGCCTTCC	AGGCCAAGCC	CAACAGTGAG	GAGATCTGGC	TGGCAGCCGT	GAAGCTGGAG	1020
TCCGAGAATG	ATGAGTACGA	GCGGGCCCGG	AGGCTGCTGG	CCAAGGCGCG	GACAGTGCCC	1080
CCACCGCCCC	GGTGTTCATG	AAGTCTGTGA	AGCTGGAGTG	GGTGCAAGAC	AACATCAGGG	1140
CAGCCCAAGA	TCTGTGCGAG	GAGGCCCTGC	GGCACTATGA	GGACTTCCCC	AAGCTGTGGA	1200
TGATGAAGGG	GCAGATCGAG	GAGCAGAAGG	AGATGATGGA	GAAGGCGCGG	GAAGCCTATA	1260
ACCAGGGGTT	GAAGAAGTGT	CCCCACTCCA	CACCCCTGTG	GCTTTTGCTC	TCTCGGCTGG	1320
AGGAGAAGAT	TGGGCAGCTT	ACTCGAGCAC	GGGCCATTTT	GGAAAAGTCT	CGTCTGAAGA	1380
ACCCAAAGAA	CCCTGGGCTG	TGGTTGGAGT	CCGTGCGGCT	GGAGTACCGT	GCGGGGCTGA	1440
AGAACATCGC	AAATACACTC	ATGGCCAAGG	CGCTGCAGGA	GTGCCCCAAC	TCCGGTATCC	1500
TGTGGTCTGA	GGCCATCTTC	CTCGAGGCAA	GGCCCCAGAG	GAGGACCAAG	AGCGTGGATG	1560
CCCTGAAGAA	GTGTGAGCAT	GACCCCCATG	TGCTCCTGGC	CGTGGCCAAG	CTGTTTTGGA	1620
GTCAGCGGAA	GATCACCAG	GCCAGGGAGT	GGTCCACCG	CACTGTGAAG	ATTGACTCGG	1680
ACCTGGGGGA	TGCCTGGGCC	TTCTTCTACA	AGTTTGAGCT	GCAGCATGGC	ACTGAGGAGC	1740
AGCAGGAGGA	GGTGAGGAAG	CGCTGTGAGA	GTGCAGAGCC	TCGGCATGGG	GAGCTGTGGT	1800
GCGCCGTGTC	CAAGGACATC	GCCAACTGGC	AGAAGAAGAT	CGGGGACATC	CTTAGGCTGG	1860
TGGCCGGCCG	CATCAAGAAC	ACCTTCTGAT	TGAGCGGTTG	CCATGGCCGG	TCTCCGTGGG	1920
GCAGGGTTGG	GCCGCATGTG	GAAGGGCTCT	GAGCTGTGTC	CTCCTTCATT	AAAAGTTTTT	1980
ATGTCTCGTG	TCAGAAAAAA	AAAGAAAAAG	AAAAAGGGGG	CGCCCGGGGG	C	2031

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(2) INFORMATION ON SEQ ID NO. 2:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1081 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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AAGACCCCGT CTCTACAAAG CAAAACGAAA AACAACAAAT GGAGTTGTGC TATGTTGTAT 60
TGCTTTGCAC AAAATTAGGA ACAGGTGTTT GACAATTGAA TTTGTTTTCT GTGAATTCTA 120
ACCTCTAAAG GCATGCTTAG AGGTCAAGGA CCTTCCTGTG TAGTTGGTGC AAAAGCAATC 180
TCCACAGGAC AGCACTGCTT CCATGCTTCA TACATCAGGA AATGAGGCCA GAACTTGAGT 240
ATTTACTAAC ACGTTTTTCA AAAGATGTCA GTGTTATACC TAAAGCTAAA AAAAAGCAAG 300
GGTTTGTGTCAT AGAGGGAACC TCTAAATAAT TTCAGGGGTA GGGGAGATGT TGTCAATAGG 360
AAATGGGATA AAATATCAAG AGACAATGAA AACACTGCCT TGACATGAGG ACCAGCAAGT 420
TTATTCTTTT CATTTTCAGT GATGTTGGGA ATGGACTGGG TTTTAAAGG GAGCTTGAAG 480
AGGGAATGTT TGACAGTCAC AGAAGGTTCC TGCAGCAGAT GCCTCTTTTA GCCATTTCTC 540
ATTTTTTTCC TCAAATTTTA CCTACTGAGG CTCAAGCCTT CACAGTGAGC TGATGGTCTC 600
TACAGGGGAG GGGAGTCTAG GGAATTTATT TGGTATTTGT AAGGCAAGAG GTGATTTCTC 660
TCTAATATAT CTGAGTTATT GCTCATTTAA AACTGTTAAG TCCAGTATAA TTTTCCCTGA 720
TATGAAAAAA TGTGCATTTT TTTCACCTAG CAACAAAGTA CCTTCTAATT TCCAATAGTC 780
CGTGAAAGTT GGGGCTGAAG TACCTAAGTG TGAATGTCTC TCCCGTTAAA CTGAGTGTAG 840
AAATCTGAAT TTTTAAAAGA GCTGTAAC TAAGTGAAGT CTTAGGAAGA AACTTTGCAA 900
ACATTTAATG AGGATACACT GTTCATTTTT AAAATTCCTT CACACTGTAA TTTAATGTGT 960
TTTATATTCT TTTGTAGTAA AACAACATAA CTCAGATTTT TACAGGAGAC AGTGGTTTTA 1020
TTTGGATTGT CTTCTGTAAT AGGTTTCAAT AAAGCTGGAT GAACTTAAAA AAAAAAAAAA 1080
A

```

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCCAAAGCGC AGGGTCAGCG ACACTTCTTC CGGCCCAACG CCGTGCATGG AGCCCATCCT 60
 GGGCCGCACG CATTACAGCC AGCTGCGCAA GAAGAGCTGA GTCGCCGCAC CAGCCGCCGC 120
 GCCCCGGGCC GGGGGGTTTC TCTAACAAAT AAACAGAACC CGCACTGCCC AGGCGAGCGT 180
 TGCCACTTTC AAAGTGGTCC CCTGGGGAGC TCAGCCTCAT CCTGATGATG CTGCCAAGGC 240
 GCACTTTTTA TTTTATTTT ATTTTATTT TTTTTTAGC ATCCTTTTGG GGCTTCACTC 300
 TCAGAGCCAG TTTTAAAGG ACACCAGAGC CGCAGCCTGC TCTGATTCTA TGGCTTGGTT 360
 GTTACTATAA GAGTAATTGC CTAAGTTGAT TTTTCATCTC TTTAACCAAA CTTGTGGCCA 420
 AAAGATATTT GACCGTTTCC AAAATTCAGA TTCTGCCTCT GCGGATAAAT ATTTGCCACG 480
 AATGAGTAAC TCCTGTCACC ACTCTGAAGG TCCAGACAGA AGGTTTTGAC ACATTCTTAG 540
 CACTGAACTC CTCTGTGATC TAGGATGATC TGTTCCCCCT CTGATGAACA TCCTCTGATG 600
 ATCTAGGCTC CCAGCAGGCT ACTTTGAAGG GAACAATCAG ATGCAAAAGC TCTTGGGTGT 660
 TTATTTAAAA TACTAGTGCT ACTTTCTGAG TACCCGCCGC TTCACAGGCT GAGTCCAGGC 720
 CTGTGTGCTT TGTAGAGCCA GCTGCTTGCT CACAGCCACA TTTCCATTTG CATCATTACT 780
 GCCTTCACCT GCATAGTCAC TCTTTTGATG CTGGGGAACC AAAATGGTGA TGATATATAG 840
 ACTTTATGTA TAGCCACAGT TCATCCCCAA CCCTAGTCTT CGAAATGTTA ATATTTGATA 900
 AATCTAGAAA ATGCATTCAT ACAATTACAG AATTCAAATA TTGCAAAAGG ATGTGTGTCT 960
 TTCTCCCCGA GCTCCCCTGT TCCCCTTCAT TGAAAACCAC CACGGTGCCA TCTCTGTGT 1020
 ATGCAGGGCT ATGCACCTGC AGGCACGTGT GTATGCACTC CCCGCTTGTT TTTACACAAG 1080
 CTGTGGGGTG TTACGCATGC CTGCTTTTTT CACTTAATAA TACAGCTTGG AGAGATTTTT 1140
 GTATCACATT ATAAATCCCA CTCGCTCTTT TTGATGGCCA CATAATAACT ACTGCATAAT 1200
 ATGGATACGC CTTATTTGAT TTAAGTAGTT CCCTAATGAT GGACTTTTAA GTTGTTCCT 1260
 TTTTTTTTCT TTTTGTCTAC TGCAAACGAT GCTATAATAA ATGTCCTTAT CAAAAATG 1318

(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 731 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

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(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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CTTGGGACAA GACTCTCACC AGCACATCAC ACACGTTCTC CTTGGAAGAG AGAAGCAGTA 60
CATCCCGGTT GAGAGGTCAC AAAGCATTAG TGGAAGAAAT GTGGTAAAGG GGGGAAGGTG 120
TTATGCGGCT GCTCCCTCCG TCCCAGAGGT GGCAGTGATT CCATAATGTG GAGACTAGTA 180
ACTAGATCCT AAGGCAAAGA GGTGTTTCTC CTTCTGGATG ATTCATCCCA AAGCCTTCCC 240
ACCCAGGTGT TCTCTGAAAG CTTAGCCTTA AGAGAACACG CAGAGAGTTT CCCTAGATAT 300
ACTCCTGCCT CCAGGTGCTG GGACACACCT TTGCAAAATG CTGTGGGAAG CAGGAGCTGG 360
GGAGCTGTGT TAAGTCAAAG TAGAAACCCT CCAGTGTGTTG GTGTTGTGTA GAGAATAGGA 420
CATAGGGTAA AGAGGCCAAG CTGCCTGTAG TTAGTAGAGA AGAATGGATG TGGTTCTTCT 480
TGTGTATTTA TTTGTATCAT AAACACTTGG AACAACAAAG ACCATAAGCA TCATTTAGCA 540
GTTGTAGCCA TTTCTAGTT AACTCATGTA AACAAGTAAG AGTAACATAA CAGTATTACC 600
CTTTCAGTGT TCTCACAGGA CATGTACCTA ATTATGGTAC TTATTTATGT AGTCACTGTA 660
TTTCTGGATT TTAAATTAA TAAAAAAGTT AATTTTGAAA AATCAAAAAA AAAAGAAAGG 720
AAGTAAAAGG A 731

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(2) INFORMATION ON SEQ ID NO. 5:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2719 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGAGACCAGG	CCCACAGAGA	ACAGGGCAAG	GAGCAGGCCA	TGTTTGATAA	GAAGGTGCAG	60
CTCCAGAGAA	TGGTAGACCA	AAGGTCGGTG	ATTTTCAGATG	AAAAGAAAGT	TGCCCTCCTC	120
TATCTAGACA	ATGAGGAGGA	GGAGAATGAT	GGGCATTGGT	TTTAATAAGC	AGAAACATTT	180
TGTTTTAATG	GCAGCCTGTT	GGCGACGTGC	CAACATCCAA	AGGCCTTAAC	TTATTTTAAG	240
AGGCCGAGGG	AGTCTATGAA	AATCTCCCCT	TTTTTACTTT	TTTAAAGAGT	ACTCCCGGCA	300
TGGTCAATTT	CCTTTATAGT	TAATCCGTAA	AGGTTTCCAG	TTAATTCATG	CCTTAAAAGG	360
CACTGCAATT	TTATTTTTGA	GTTGGGACTT	TTACAAAACA	CTTTTTTCCC	TGGAGTCTTC	420
TCTCCACTTC	TGGAGATGAA	TTTCTATGTT	TTGCACCTGG	TCACAGACAT	GGCTTGCATC	480
TGTTTGAAAC	TACAATTAAT	TATAGATGTC	AAAACATTAA	CCAGATTAAA	GTAATATATT	540
TAAGAGTAAA	TTTTGCTTGC	ATGTGCTAAT	ATGAAATAAC	AGACTAACAT	TTTAGGGGAA	600
AAATAAATAC	AATTTAGACT	CTAAAAAGTC	TTTTCAAAAA	GAAATGGGAA	ATAGGCAGAC	660
TGTTTATGTT	AAAAAAATTC	TTGCTAAATG	ATTTCATCTT	TAGGAAAAAA	TTACTTGCCA	720
TATAGAGCTA	AATTCATCTT	AAGACTTGAA	TGAATTGCTT	TCTATGTACA	GAACCTTAAA	780
CAATATAGTA	TTTATGGCGA	GGACAGCTGT	AGTCTGTTGT	GATATTTTAC	ATTCTATTTG	840
CACAGGTTCC	CTGGCACTGG	TAGGGTAGAT	GATTATTGGG	AATCGCTTAC	AGTACCATTT	900
CATTTTTTGG	CACTAGGTCA	TTAAGTAGCA	CACAGTCTGA	ATGCCCTTTT	CTGGAGTGGC	960
CAGTTCCTAT	CAGACTGTGC	AGACTTGCGC	TTCTCTGCAC	CTTATCCCTT	AGCACCCAAA	1020
CATTTAATTT	CACTGGTG	AGGTAGACCT	TGAAGACAAT	GAAGAGAATG	CCGATACTCA	1080
GACTGCAGCT	GGACCGGCAA	GCTGGCTGTG	TACAGGAAAA	TTGGAAGCAC	ACAGTGGACT	1140
GTGCCTCTTA	AAGATGCCTT	TCCCAACCCCT	CCATTCATGG	GATGCAGGTC	TTTCTGAGCT	1200
CAAGGGTGAA	AGATGAATAC	AATAACAACC	ATGAACCCAC	CTCACGGAAG	CTTTTTTTGC	1260
ACTTTGAACA	GAAGTCATTG	CAGTTGGGGT	GTTTTGTCCA	GGGAAACAGT	TTATTAAATA	1320
GAAGGATGTT	TTGGGGAAGG	AACTGGATAT	CTCTCCTGCA	GCCCAGCACC	GAGATACCCA	1380
GGACGGGCTT	GGGGGGCGAG	AAAGGCCCCC	ATGCTCATGG	GCCGCGGAGT	GTGGACCTGT	1440
AGATAGGCAC	CACCGAGTTT	AAGATACTGG	GATGAGCATG	CTTCATTGGA	TTCAATTTAT	1500
TTTACACGTC	AGTATTGTTT	TAAAGTTTCT	GTCTGTAAAG	TGTAGCATCA	TATATAAAAA	1560
GAGTTTCGCT	AGCAGCGCAT	TTTTTTTAGT	TCAGGCTAGC	TTCTTTCACA	TAATGCTGTC	1620
TCAGCTGTAT	TTCCAGTAAC	ACAGCATCAT	CGCACTGACT	GTGGCGCACT	GGGGAATAAC	1680
AGTCTGAGCT	AGCACCAACC	TCAGCCAGGC	TACAACGACA	GCACTGGAGG	GTCTTCCCTC	1740
TCAGATTAC	CTGGAGGCC	TCAGACCCCC	AGGGTGCACG	TCTCCCCAGG	TCCTGGGAGT	1800
GGCTACCGCA	GTAGTTTCTG	GAGAGCACGT	TTTCTTCATT	GATAAGTGGA	GGAGAAATGC	1860
AGCACAGCTT	TCAAGATACT	ATTTTAAAAA	CACCATGAAT	CAGATAGGGA	AAGAAAGTTG	1920
ATTGGAATGG	CAAGTTTAAA	CCTTTGTTGT	CCATCTGCCA	AATGAACTAG	TGATTGTCAG	1980
ACTGGTATGG	AGGTGACTGC	TTTGTAAGGT	TTTGTCGTTT	CTAATACAGA	CAGAGATGTG	2040
CTGATTTTGT	TTTAGCTGTA	ACAGGTAATG	GTTTTTGGAT	AGATGATTGA	CTGGTGAGAA	2100
TTTGGTCAAG	GTGACAGCCT	CCTGTCTGAT	GACAGGACAG	ACTGGTGGTG	AGGAGTCTAA	2160
GTGGGCTCAG	TTTGATGTCA	GTGTCTGGGC	TCATGACTTG	TAAATGGAAG	CTGATGTGAA	2220
CAGGTAATTA	ATATTATGAC	CCACTTCTAT	TTACTTTGGG	AAATATCTTG	GATCTTAATT	2280
ATCATCTGCA	AGTTTCAAGA	AGTATTCTGC	CAAAAGTATT	TACAAGTATG	GACTCATGAG	2340
CTATTGTTGG	TTGCTAAATG	TGAATCACGC	GGGAGTGAGT	GTGCCCTTCA	CACTGTGACA	2400
TTGTGACATT	GTGACAAGCT	CCATGTCCTT	TAAAATCAGT	CACTCTGCAC	ACAAGAGAAA	2460
TCAACTTCGT	GGTTGGATGG	GGCCGGAACA	CAACCAGTCT	TTTTGTATTT	ATTGTTACTG	2520
AGACAAAACA	GTAATCACTG	AGTGTTTTTT	AGTTTCCTAC	TGGTGGTTTT	GATATTGTTT	2580
GTTTAAAGATG	TATATTTAGA	ATGACATCAT	CTAAGAAGCT	GATTTTGCTA	AACTCCTGTT	2640
CCCTACAATG	GGAAATGTCA	CAAGAATGTG	CAAAAATAAA	AATCTGAGGA	AAAAACCCAA	2700
AAAATTCCTA	AAGAGAATG					2719

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(2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

gggccggggca gccagctga aggcaataag ctgggctcac cgctgcagca gagttctgtg 60
ctagccgggc ataggggcga gagaaggccc agaggcgacg tcagagagaa gcaactgcgc 120
cccgggtgaag agaagctcgc ccatacccg ctgggagcca gctttcagtg aagatggcag 180
ggccagaact gttgcttgac tccaacatct gcctctgggt ggtcctaccc atcgttatca 240
ctcttcgtag acatgatccg ccactacgtg tccatcctgc tggagagcga caagaagctc 300
accaggaac aagtatctga caggggacga ggcaccacaca gtccctctcc cataagcctg 360
ccaagaagat tgatgtggcc cgtgtaacgt ttgacctgta caagctgaac ccacaggact 420
tcattggctg cctgaacgtg aaggcgactt tttatgatac atactccctt tcctatgatc 480
tgcaactgctg tggggccaag cgcatacga aggaagcttt ccgctgggcc ctcttcagca 540
tgcaggccac aggccacgta ctgcttgga cctcctgtta cctgcagcag ctctcgatg 600
ctacggagga agggcagccc cccaagggca aggccctcct ccttatcccg acctgtctga 660
agatactgca gtgaaagccc aagtccttgg aagctttccc cagtgaagga ctgactgggg 720
gcctcacgct taactggtag tgcccacaag cctggcagct gtagagccgc gaacctcccc 780
acacctccct caccgcgag gaccctgagt gaggaggagg agctggaaac ctgggggtggg 840
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gcagtcgggc ctacaggtc gtactttcat ggtgctctct accttctggc ccccatccca 1020
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attattgatg ctgatgtaaa aaaaaaa

```

1107

(2) INFORMATION ON SEQ ID NO. 11:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

09646569.092000

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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gtgaatatgt gtgtatatgt gtgtgtatgt gtgtgtgggg tttggggtag aaggaggagga 60
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taagtgggct tttatgctaa aagcctctgg ggatatctgt tttgaaaata aagatagggtg 180
tccccctcctt gctgtcatct agcccagaca ctctgcttgc tctctggctg tctgctccct 240

gggaaggctt taggaggacc acccaggaca ggatgaccat gctgccatct gctctggagc 300
tgggtctcag tgcagaggga cagtgactgt ggatgggttg agtctctggt gggaggtgag 360
gatagaagtg ataaagagct aagaggagct tctgggagcc ttggaggagg tcagtcttgc 420
agtgggtgaag ccaggacata ggagatggag cagggtctgt agaggaggag attctgagga 480
ggatgcaggg gaaatcttgt ctgttaatga aataggggtg ggggtggggtt tgggggtggg 540
tggtcattgc cgtttgagct gctgattttc atgagtcgcc ttcaaaactc tcgtgtaggg 600
ttgacaatgt ggggggggtg gggatccagc ttattctttt attttcaagt ccattcttgg 660
ggctgggtgg gaggcaggag aatacccctc cctaagccct tagtgtgtgc cgagcttgct 720
ttgtgatgtt ggcaggggag gggagacctg ggtgggtgact gagttccctt tatcaaacc 780
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tctgtgtttc cccctgccct ccagactgt gtggccagtt gaaagtgtct ggtttgtgtt 900
catctctccc tcatttcttg agcagggcct gagaccctgc cacatctcct atgctctgca 960
tccacgcctc ttttgacat taaagggttg ttgatgcaaa acaactttac aacgggggtgg 1020
cttggggaag cctgggggtg gccggcttat ggggttgccg cg 1062

```

(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1471 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

09645569 "092000

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
attacaggca tgagccactg taccagcctt ttccttataa aattcaaaga gaaaatttct 60
acacctttat ccttcaaata aaacaagtgc tcagttctta ccgtgccctt gcaagggtcta 120
tatgtaaaag aaatctgaaa tttagctgta gaataaaact tgataaataa aaagaaaaaa 180
catacatttc tccagttggt ttgctctttg cttgttgaag taataaacgg ttttaaagag 240
aaaataacttg ctgtaaaccc ccagtgccctt caactctttt ggcagaatat ttttaaagaa 300
atccagcaag caaactttga ggtgctaata aaagtaaagg aagggtggtat ttctagtttt 360
ggcagaaatg aaaagtgtct cacaagagac atcactaccc acgtgggggtc tggctgcttt 420
ctaccaaaga catttagaga agaagtgaat tgagtcaggg tgatggtgaa cactacatat 480
tttatagatg gtttaagtga gaattaatta tgtttatcat ggatggctac taataccaag 540
ctcatgattg ttgcagcctc aacgtcttag gcagtaaaac ttgtctgcag cactaaaggg 600
ggagaaaacc ttatatatttg caaactgtcc attcggtaaa tttattgtaa cctaatacca 660
aaaactgccg tttttcatat tatttcccca cctcctactt tttttttttt tttttgctac 720
ttgtaaaata accccttcta gaaaataagc attaactgga atgtttcaaa caattttgct 780
```

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tcattttact atcagccact agtgaactct tacagagatg tacatttaag ataaaattag 840
cttgtgctaa gtgtttttaa aacattgttt actgttaaag ggaattgca cattatat 900
aactgggatt gtcctctccc tcagttcttt aaaaaacaag agtcaaggct cacaccaact 960
tgtaggctgt gggagctttg ccataggtag atacaatgta gaagtatact tttttaaagc 1020
atgaagaaga caaggaaact cattataatg taccaggtag aggacattat tattcaaagg 1080
attatgcaca gctcagtga gatgaagtta caatttttct cgcagctttg ttgctattat 1140
tttcttctgc ataaatgtat gctcatttca ttatgtgcct tgctccctga ttgtgcaaag 1200
cttatatata tatatatata gatagataga tagatagata gatatatgag agagatatat 1260
tcagtactac tgaggatggt tttctgagga tgtttttgtt ctgctggatt aagttatttt 1320
ccaagttact cttgccagtt atgtcagtaa actattgtaa tggcttagca cactagtcgt 1380
acagtcagtg taaatgtttt tcattttacat gttttcatta tatcagctta tcaaattcct 1440
aataaaaaaa attcatagat ttcattttaa c 1471
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(2) INFORMATION ON SEQ ID NO. 13:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2738 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

000260"6954560

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

gctccgtgcc agcatgctac cctgggaggc acatccaggc ttgggaaacg ggggtgtcct 60
 ggatctcatg actccagcag caccagctgc tctctttcct ctccaagta gacttccgtt 120
 cccccccac ttgggtgttt ttgtttgttt tagcaattca gagctcaaga taaagacctt 180
 aaagataact ttgtgtgtct ctccctttct aggtatttgc ataggaatca gaggagttaa 240
 tcttgtctct tctcacaggt ttgaatcttc agacaaactt ctgggaggac tccgtccatg 300
 cctcgagca gatgttccct gtcaatcagt aggc aaattg gctacccatt ctcccagaa 360
 atctcaccag tgtgctcact gtgagaagac gttcaaccgg aaagaccacc tga aaaacca 420
 cctccagacc caccagccca acaaaatggc ctttgggtgt gaggagtgtg ggaagaagta 480
 caacaccatg ctgggtcata agaggcacct ggccctccat gcggccagca gtggggacct 540
 cacctgtggg gtctgtgccc tggagctagg gagcaccgag gtgctactgg accacctcaa 600
 agcccatgcg gaagagaagc cccctagcgg aaccaaggaa aagaagcacc agtgcgacca 660
 ctgtgaaaga tgcttctaca cccggaaggga tgtgcgacgc cacctgggtg tccacacagg 720
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 ccggcatacc aagaagaccc actcacagga gctgatgaaa gagagcttgc agaccggaga 840
 ccttctgagc accttcaca ccattctgcc ttcatccaa ctgaaggctg ctgccttgcc 900
 tcctttccct ttaggagctt ctgccagaa cgggcttgca agtagcttgc cagctgaggt 960

ccatagcctc accctcagtc cccagaaca agccgcccag cctatgcagc cgctgccaga1020
 gtccttgggc tccctccacc cctcggtatc ccctggctct cctccgccac cccttccca1080
 tcacaagtac aacaccactt ctacctcata ctccccactt gcaagcctgc ccctcaaagc1140
 agatactaaa ggtttttgca atatcagttt gtttgaggac ttgcctctgc aagagcctca1200
 gtcacctcaa aagctcaacc caggttttga tctggctaag ggaaatgctg gtaaagtaaa1260
 cctgcccgaag gagctgcctg cagatgctgt gaacctaaaca atacctgcct ctctggacct1320
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 aatctgtcct gagtgttcat gctttgtacc aaatttaatg aacgcgtgtt ctgtaatcaal800
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 aagactaaac tggttgtcag ttacatctga cagaaaaaaa aaaaaaatca ctgtgtaacc2280
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 aacaagaatt ttctttgtct tgtctagctt aaactactac tcaagctgct taagttctta2460
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 tagaggcttt tccgtaaaaa tatatcttac atataataaa cttttcaaat cttgcaaaaa2700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2738

09646569 092000

(2) INFORMATION ON SEQ ID NO. 14:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1710 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

cgccgcgggcc cctcctccca gagcggcagc cttttccgc gcgtgctgcc ttgcgcgctc 60
gggcccggccg ggggaaaaca tggcgtctgc cctggagcag ttcgtgaaca gtgtccgaca 120
gctctcagct caagggcaaa tgacacagct ttgtgaactg atcaacaaga gtggggaact 180
ccttgcgaaq aacttatccc atctggacac tgtgctcggg gctctggatg tacaagaaca 240
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cgaaacgcta ttctcacagg ttcagctctt catcagcact tgtaatgggg agcacattcg 360
atatgaaca gacacttttg ctgggctttg ccacagcta acaaatgcac ttgtggaaag 420
aaaacagtga caacataaga tccaatgtgc tgccatcttt gagaacttat ctgaaagaga 480
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cagatgaata caaaccagct gacctcaata catgctgac tctgccagct ttgtttgcta 600
gcaaaatgct ttaagcctgc ccttccatat cttgacgtgg atatgatgga tatctgtaaa 660
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tatactgggc tgaagaactt tgaaagagct ctctactttt atgaacaggc tataactact 780
cctgccatgg cggtcagtca tatcatgttg gaatcatata aaaagtatat tttagtgtct 840
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ccctcagaac tccgaaacct ggtgaataag cacagtgaac ccttcactcg cgataacaac 1020
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aaccagaagg acggtatggt cagtttccat gataaccctg aaaaatataa taaccagacc 1260
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gccatggacc aggagatcac agtgaaccct cagtttgtac aaaagagtat gggctcaca 1380
gaagatgatt caggaaacaa accatccagt tattcttgaa actaacatcc atcctgagct 1440
aaacaagaga aactaccatc ttggccagtg acaagtgttc ggagggcagc agagaggacc 1500
aagcctgtgt cacctggaga ctaagaaatt aagttttgtt ttgacatctt cagtcctgtg 1560
tgctttcaga aaaccatttt ctctgcaaag aaaggaaaca gatttgcaaa ctttaaagtc 1620
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aagttgcttg aacattaaaa aaaaaaaaaa

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1710

09646569 "092000

(2) INFORMATION ON SEQ ID NO. 15:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3159 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

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tcgagaccct caatctctat ttccacatcc agtggtttcag gtgtggaatt tgtaaaggcc 180
agcttgagga tgcagtgagt gggacggatg ttaggattcg aaatggtctc ctgaactgta 240
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aagcttcggg atcactcacc atttctttac tgagagtgtc ccctggcaac tgcttaacaa 360
aatcccaagc tcaggggctt ctcagcattt acctaatttc tgaaaggctc ttctgaaagg 420
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cttcttttgg aattagctaa atgatgcaat aaacctgttt tgttttagaa tgcctaggaa 660
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caagttctcc ttaagggcct gaagcacagg tgtccaaaga aaagcgtaa gtccatctta 1320
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ctagcgatta tttattacat gctagatggg ttctttgcat gtgggttcca tataggtgca 1860
gaaatttctc cagccactgg agggatttgc accatatattg tcatttggat gagctgttat 1920
tagattgaaa tctacacatc atttcattaa aaattgtgcc ttagaaaacg caaagctgtt 1980
gcacatggcg ataaattatg gatgcagtac attgaagaga gatgaagtca cttccaagtt 2040
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tgcatgatat tagcagagta ccactagtaa tgcacaaaca tgtacaatat gggtattcat 2280
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ctcattgtac atgtattgaa gctagaatcg agtcaagaaa aataaagccc cattctccaa 2460
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tttctaaatt ctaattgcca actgtttcta tttatatattg atttatattt catttgaggt 2580
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caaaactgaaa tgatccacct catatgtgag tccgtccaaa agatgttact gctctgggtg 3000
ggccagtgtt ctatatcggt tatactaact ttcattttaa gtattttatt taaaatgcct 3060
ctgagaaaca gtaaaaaata aaaacaacaa gttgtctaaa atgcaacagc ttttatagta 3120
aatgtacatt tataaataaa atactcaaat caaaaaaaa

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3159

(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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ctagcttggt tcctttccaa gtgtcaaata ggacacccat cttaccggcc aatgtccaaa 180
attacggttt gaacataatt ggagaacctt tccttcaagc agaaacaagc aactgaggga 240
aaaagaaaca caacaatagt ttaagaaatt ttttttttaa ataaaaaaaa ggaaaagagg 300
aagactggac aaaacaacac aaaggcagaa aggaaagaaa ctgaagaaa aagataatag 360
accagcaatt gcagcactta caatcactaa ttcccttaag gttgaaactg taatgacata 420
aaaagggtcg atgataattt actgatggta gatcgagcc cctgcaacgt agcctttgtt 480
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tctagatgcc ttaatatatt catgataagc tagttttatt ggtttagtat tcttgttgtt 600
tacgcattga atcactattc ctggttatct caccaacgaa ggctaggagg cggcgtcaga 660
ggtgctgggt gacagagcca tgagccagcc attttataag cactctgatt tctaaaagt 720
aaaaaaaaata tatgaaatct ctgtagcctt tagttatcag tacagattta ttaattttcg 780
gcccttaacc cagccttttc cagtgtgtaa ccagtttga aatcttaaaa aaagaaaaaa 840
tgaaaaaaa aggaaaaaaa gaaaaaagga aaaaaacagt ttgaacacaa aggctctatg 900
gaagaaatgc ctctatgtag gtgaagtgtt ctctctgcat gcaacagtaa aaattaatat 960
aatattttcc ccacaaaaga aacacttaac agaggcaagt gcaatttata aatttatatc 1020
taaaggggaa tcatgattat aagtccttca gcccttggac tctaaattga ggggattaaa 1080
aagaatttaa aataattttg aacgaattta tttcccctc agtttttgag ggcattaaaa 1140
aggcattaaa tcaagacaaa tcatgtgctt gagaaaaata aaattaatga aaacacagca 1200
cttatgttgg tttagctgca gctccttgg aggtagaatt tatttattta aaattactgg 1260
ttgcatcaag aacctatagg gtgtacaaaa ggttctataa aatctgcatt atagagacaa 1320
agaggcaggc aaatccatgt cacaagggtt aagcttacag ttacaaact gggaacgcc 1380
gggtgtagga tataaaaacg cactcttgag aaaacaaatg taatcagggt gctgaaaact 1440
tgcatggtgc tttcagacat tagccttgtt caacaaattt cttgtattga cagatccata 1500
gtgtgcatgg gcagacacat tttgcctcta tgtctcttaa aattttaatt aaaaataact 1560
ttccagtaa tcctaatttg cacgaagata taatgtccac attacgtgcc ttgccttga 1620

atctaaaaaa caaaaaacaa aaaagaaaa agaacaaaaa atacaacaaa gtgacatcac 1680

```

000260"6954960

(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1722 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260 " 69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

cattgtttgc caaaatccca ggcagcatgg acctcagtct tctctgggta cttctgcccc 60
 tagtcacccat ggccctggggc cagtattggcg attatggata cccataccag cagtatcatg 120
 actacagcga tgatgggtgg gtgaatttga accggcaagg cttcagctac cagtgtcccc 180
 aggggagcgt gatagtggcc gtgaggagca tcttcagcaa gaaggaaggt tctgacagac 240
 aatggaacta cgccctgcatg cccacgccac agagcctcgg ggaaccacag gagtgtctgg 300
 gggaggagat caacagggct ggcatggaaat ggtaccagac gtgctccaac aatgggctgg 360
 tggcaggatt ccagagccgc tacttcgagt cagtgtctgga tcgggagtg gagtgttact 420
 gttgtcgcta cagcaagagg tgcccatatt cctgtctggc aacaacagaa tatccaggtc 480
 actatggtga ggaaatggac atgatttctt acaattatga ttactatata cgaggagcaa 540
 caaccacttt ctctgcagt gaaagggatc gccagtggaa gttcataatg tgccggatga 600
 ctgaatacga ctgtgaattt gcaaatgttt agatttgcca cataccaaat ctgggtgaaa 660
 ggaaaggggc cggggacagg aggggtgtcca catatgttaa catcagttgg atctcctata 720
 gaagtttctg ctgtctctct tcttctctcc tgagctggta actgcaatgc caacttctctg 780
 ggcttttctg actagtatca cacttctaataaaaatccaca attaaacat gtttctcact 840
 tttcacatgt ttcatagcaa ctgctttata tgactgatga tggcttctct gcacaccaca 900
 tatacagtgc gcatgcttac agccgggctt ctggagcacc agctgcagcc tggctactgc 960
 tttttactgc agaatgaact gcaagttcag catagtggag gggagaggca gaactggagg 1020
 agaggtgcag tgaaggttct ctacagctaa gcctgtttga atgatacgta ggttccccac 1080
 caaaagcagg ctttctgccc tgagggacat cttccactc ccctgtctca catgagccat 1140
 gcatgcttag caatccaagt gcagagctct ttgctccagg agtgaggaga ctgggaggtg 1200
 aaatggggaa atggaagggt ttggaggcag agctgaaaac aggggttgaa ggatttctctg 1260
 aattagaaga caaacgttag catacccagt aaggaaaatg agtgcagggg ccaggggaac 1320
 ccgtgaggat cactctcaaa tgagattaaa aacaaggaa cagagaatgg tcagagaatg 1380
 ggattcagat tgggaacttg tggggatgag agtgaccagg ttgaactggg aagtggaaaa 1440
 aggagtttga gtcactggca cctagaagcc tgcccacgat tcctaggaag gctggcagac 1500
 accctggaac cctggggagc tactggcaaa ctctctctgga ttgggcctga tttttttggt 1560
 gggaaaggct gccctgggga tcaactttcc ttctgtgtgt ggctcaggag ttcttctgca 1620
 gagatggcgc tatcttttct cctcctgtga tgtcctgctc ccaaccattt gtactcttca 1680
 ttacaaaaga aataaaaaata ttaacgttca ctatgctgaa aa 1722

(2) INFORMATION ON SEQ ID NO. 19:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1612 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

09645569 "092000

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

ggccatggaa attaaagttg aaaaagactt gaagactgga gaaagtacag ttctgtcttc 60
aattacctct gccatcagat gacttttaaag gtacaggaat aaaagtttat gatgatgggc 120
aaaagtcagt gtatgcagta agttctaata acagtgcagc atacaatggc accgatggcc 180
tggcaccagt tgaagtagag gaacttctaa gacaagcctc agagagaaac tctaaatccc 240
caacagagta tcatgagcct gtatatgcca atccctttta caggcctaca accccacaga 300
gagaaacggt gacccttgga ccaaactttc aagaaaggat aaagattaaa actaatggac 360
tgggtatttg tgtaaatgaa tccatacaca atatgggcaa tggcttttca gaggaaaggg 420
gaaacaactt caatcacatc agtcccatc cgccagtgcc tcatccccga tcagtgattc 480
aacaagcaga agagaagctt cacaccccg caaaaaggct aatgactcct tgggaagaat 540
cgaatgtcat gcaggacaaa gatgcacct ctccaaagcc aaggctgagc cccagagaga 600
caatatttgg gaaatctgaa caccagaatt cttcaccac ttgtcaggag gacgaggaag 660
atgtcagata taatatcggt cattccctgc ctccagacat aaatgataca gaaccgggtga 720
caatgatttt catgggggat cagcaggcag aagacagtga agaagataag aagtttctga 780
caggatatga tgggatcatc catgctgagc tggttgtgat tgatgatgag gaggaggagg 840
atgaaggaga agcagagaaa ccgtcctacc accccatagc tccccatagt cagggtgtacc 900
agccagccaa accaacacca ctctctagaa aaagatcaga agctagtctt catgaaaaca 960
caaatacata atccccccac aaaaattcca tatctctgaa agagcaagaa gaaagcttag1020
gcagccctgt ccaccattcc ccatttgatg ctgagacaac tggagatggg actgaggatc1080
catccttaac agctttaagg atgagaatgg caaagctggg aaaaaagggtg atctaagagt1140
tgtaccacct atataaacat ctttgaaga agaaactaag aagcatttgc aaatttctct1200
tctggatatt ttgtttatit tttctgaagt caaaaaaatt atcattacag tgtaccatat1260
taagccatgt gaataagtag tagtcattat ttgtgaaaaa tccccaaaaa gctggggaaa1320
acaaatgtgt aacttttcca gttacttgac acgattcagt gggggaaaaa cagcattttt1380
tattctattg ataccaaagc atttctaata agagcttggt aaatttaaga ataaagttat1440
ttaaataata aagagtatag tatattaact ggcattgtaa ttttgatgat acaaagattg1500

aaagatcata ggaaagcatt gcccttcac acagaagtat tcaactctga caaataaatal1560
tgtcatcctg aattaaatat gccttaataa aagtacatcc tcttgctaaa aa 1612

```

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 1304 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

000260" 69594960

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

agaagttccc aggcatacgg cttacctgg ctacactggc aggcaacttc cgaatgcctg 60
tggtgaggga gtacctgatg tctggaggta tctgccctgt cagccgggac accatagact 120
atttgctttc aaagaatggg agtggcaatg ctatcatcat cgtggtcggg ggtgcggtg 180
agtctctgag ctccatgcct ggcaagaatg cagtcaccct gcggaaccgc aagggctttg 240
tgaaactggc cctgcgtcat ggagctgacc tggttcccat ctactccttt ggagagaatg 300
aagtgtacaa gcagggtgatc ttcgaggagg gctcctgggg ccgatgggtc cagaagaagt 360
tccagaaata cattggtttc gccccatgca tcttccatgg tcgaggcctc ttctcctcgg 420
acacctgggg gctgggtgcc tactccaagc ccataccac tggtgtggga gagcccatca 480
ccatcccca gctggagcac ccaaccagc aagacatcga cctgtaccac accatgtaca 540
tggaggccct ggtgaagctc ttcgacaagc acaagaccaa gttcggcctc ccggagactg 600
aggtcctgga ggtgaactga gccagccttc ggggccaatt ccctggagga accagctgca 660
aatcactttt ttgctctgta aatttggaag tgtcatgggt gtctgtgggt tatttaaaag 720
aaattataac aattttgcta aaccattaca atgttaggtc ttttttaaga aggaaaaagt 780
cagtatttca agttctttca cttccagctt gccctgttct aggtggtggc taaatctggg 840
cctaactctg gtggctcagc taacctctct tcttcccttc ctgaagtgac aaaggaaact 900
cagtcttctt ggggaagaag gattgccatt agtgacttgg accagttaga tgattcactt 960
tttgcccta gggatgagag gcgaaagcca cttctcatac aagccccttt attgccacta1020
ccccacgctc gtctagtcct gaaactgcag gaccagtttc tctgccaagg ggaggagttg1080
gagagcacag ttgccccgtt gtgtgagggc agtagtaggc atctggaatg ctccagtgtg1140
atctcccttc tgccaccctt acctaccccc tagtcactca tatcgagacc tggactggcc1200
tccaggatga ggatgggggt ggcaatgaca gcctgcaggg gaaagagctt tcgcccgtgg1260
acgattttag ggggggtttc gccaccagtt ggtgtggggg gtta 1304

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(2) INFORMATION ON SEQ ID NO. 22:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 1533 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

000260" 69594960

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

gcgaggagct ggcacgcagc cagggccttt gctcaagaag ccataccagc caagaattaa 60
aatctctaaa acatcagtggt atggtgatcc ccactttggt gtggatttcc cctgagcag 120
actcaccgtg tgcttcaaca ttgatgggca gcccggggac atcctcaggc tggctctga 180
tcacagggac tctggtgtca cagtgaacgg agagttaatt ggggcacccg cccctccaaa 240
tggccacaag aaacagcgca cttacttgcg cactatcacc atcctcatca acaagccaga 300
gagatcttat ctcgagatca caccgagcag agtcatcttg gatggtgggg acagactggt 360
gctcccttgc aaccagagtg tgggtggtgg gagctggggg ctggaggtgt ccgtgtctgc 420
caacgccaat gtcaccgtca ccatccaggg ctccatagcc tttgtcatcc tcatccacct 480
ctacaaaaag ccggcgccct tccagcgaca ccacctgggt ttctacattg ccaacagcga 540
gggcctttcc agcaactgcc acggactgct gggtcagttc ctgaatcagg atgccagact 600
cacagaagac cctgcagggc ccagccagaa cctcactcac cctctgctcc ttcaggtggg 660
agaggggctt gaggccgtcc taacagtga aggccaccaa gtcccagtg tctggaagca 720
aaggaagatt tacaacgggg aagagcagat agactgctgg tttgccagga acaatgccgc 780
caaactgatt gacggggagt acaaggatta cctggcatcc catccatttg acacagggat 840
gacacttggc cagggaatgt ccaggagagc ctgaagctgg cagccttaaa gatgcaagt 900
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tcagctcctg gcaattagct ggactccatg acccaccctt ggtgcagcat agatccgacg 1020
tctgtctggg cgaagggtag ggggtgggtg gggcggaag cctgagtgc aatgtcattt 1080
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ggtcatagct aaatgcaaca aagtctgtat cttgtcccaa cctgcttttc tgttctgtta 1200
gcatatcata aagtaagcct ttctggtgaa ggaaggttgc tatgaaactt ttttcttgg 1260
tggaatggc caagtttagg cactctgctt tttgccttac actaatgctt agaaagctgt 1320
cttttcagtg gtgttgacg cccagatgt gtggccaacc tctgctgcaa aggaatctct 1380
tgctgagtc aggccaccaa tcaggcaaat agccataca tttgatcgtt gtaaaccatg 1440
aagtcttttc ttgcaagacg tttttcttct gctgtggtat cttgccctta aaaattagtt 1500
ttcattaaaa agaaatttga ttgaaaataa aaa

```

(2) INFORMATION ON SEQ ID NO. 23:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 1304 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

0964559 "092000

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

caagtgtgag ccaccacacc tggcctggaa ggaacctctt aaaatcagtt tacgtcttgt 60
at ttgttct gtgatggagg aactggaga gagttgctat tccagtcaat catgtcgagt 120
cactggactc tgaaaatcct attggttcct ttat ttattt tgagtttaga gttcccttct 180
gggtttgtat tatgtctggc aaatgacctg ggttatcaat tttcctccag ggtagatca 240
tagatcttgg aaactcctta gagagcattt tgctcctacc aaggatcaga tactggagcc 300
ccacataata gatttcattt cactctagcc tacatagagc tttctgttgc tgtctcttgc 360
catgcacttg tgcggtgatt acacacttga cagtaccagg agacaaatga cttacagatc 420
ccccgacatg cctcttcccc ttggcaagct cagttgccct gatagtagca tgtttctgtt 480
tctgatgtac ctttttctc ttcttctttg catcagccaa ttcccagaat tttcccaggc 540
aattttaga ggacctttt gggttcctat atgagccatg tcctcaaagc ttttaaact 600
ccttgctctc ctacaatatt cagtacatga ccactgtcat cctagaaggc ttctgaaaag 660
aggggcaaga gccactctgc gccacaaagg ttgggtccat cttctctccg aggttgtgaa 720
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aagctgcttt ctagatctct cccagtggag catggagggtg tttctgaatt ttgtctacct 840
cacagggatg ttgtgaggct tgaaaaggtc aaaaaatgat ggccccttga gctctttgta 900
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aggcaaaactt cctgctacac atgccctgaa tgaattgcta aatttcaaag gaaatggacc1140
ctgcttttaa ggatgtacaa aagtatgtct gcatcgatgt ctgtactgta aatttcta1200
ttatcactgt acaaaagaaaa ccccttgcta ttttaatttg tattaagga aaataaagt1260
ttgtttgtta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1304

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(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2403 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002269 6954569 092000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

gtccctggcg ccctgccttt agccgtgggg ccccccacctc caccctctgg gtttcctagg 60
 aatgtccagc ctccggagacc ttcacaaagc cttgggaggg tgatgagtgc tggtcctgac 120
 aagaggccgc tggggacact gtgctgtttt gtttcgtttc tgtgatctcc cggcacgttt 180
 ggagctggga agaccacact ggtggcagaa tcctaaaatt aaaggaggca ggctcctagt 240
 tgctgaaagt taagggaatgt gtaaaacctc cacgtgactg tttggtgcat cttgacctgg 300
 gaagacgcct catgggaacg aacttggaca ggtgttgggt tgaggcctct tctgcaggaa 360
 gtccctgagc tgagacgcaa gttggctggg tggtcacac cctggctctc ctgcaggctc 420
 acacaccttc caggcctgtg gcctgcctcc aaagatgtgc aagggcaggc tggctgcacg 480
 gggagagggg agtattttgc cgaaatatga gaactggggc ctctgtctcc caggagctc 540
 cagggccctt ctctcctccc acctggactt ggggggaact gagaaacact ttcctggagc 600
 tgctggcttt tgactttttt tgatggcaga agtgtgacct gagagtccca ccttctcttc 660
 aggaacgtag atgtcggggg gtcttgcctt ggggggcttg gaacctctga aggtggggag 720
 cggaacacct ggcctccttc cccagcactt gcattaccgt ccctgtctct cccagggtgg 780
 gacagtggcc caagcaaggc ctcaactcga gccacttctt caagagctgc ctgcacactg 840
 tcttgagca tctgccttgt gcctggcact ctgccggtgc cttgggaagg tcggaagagt 900
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 tgggacctgt cgtctcagcc tgttggtttc tcctcattgc ctcaaaccct ggggtaggtg 1020
 ggacgggggg tctcgtgccc agatgaaacc atttggaaac tcggcagcag agtttgtcca 1080
 aatgacctt ttcaggatgt ctcaaagctt gtgccaaagg tcacttttct ttcctgcctt 1140
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 agagctttta aagaatgcat gtttttttcc tgggtggaat tgagtaggaa ctgaggctgt 1320
 gcttcaggta tggtaacaat aagtggggga ttttcatgct gaaccattca agccctcccc 1380
 gccggttgca cccacttttg ctggcgtctg ctggagagga tgtctctgtc cgcattcccc 1440
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 gatttgacat ggaaggcctg ttgctttgct cttgagaata gtttctcgtg tccccctcgc 1620
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 ttgaggggac attggacggg ggccgggggc gggggttggg tttgagctac agtcatgaac 1920
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 ttaactttgc ctattttgtt ttgggtgagt ttccccctc cttattctgt cctgagacca 2040
 cgggcaaagc tcttcatttt gagagagaag aaaaactgtt tggaaccaca ccaatgatat 2100

 ttttctttgt aatacttgaa atttattttt ttattatttt gatagcagat gtgctattta 2160
 tttatttaat atgtataagg agcctaaaca atagaaagct gtagagattg ggtttcattg 2220
 ttaattgggt tgggagcctc ctatgtgtga cttatgactt ctctgtgttc tgtgtatttg 2280
 tctgaattaa tgacctggga tataaagcta tgctagcttt caaacaggag atgcctttca 2340
 gaaatttgta tattttgcag ttgccagacc aataaaaatac ctggttgaaa taaaaaaaaa 2400
 aaa

2403

000260"6954460

(2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2517 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260"69594560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

cagagtga aa ccttgtgc ct ggtgacaa gtccctccaa agtgctcttc cttctgggtt 60
attcaagcca aatatctggg ttccccctc tcctcattcc ctagcaaacc ccaattatct 120
tccaagatag gagatatttc ccatccccct cttttgtaaa tatctcatct ccactggag 180
agcccaggag cctattcctg gcatggatgt tctgtccaca cttgaggctg ggcggtgtat 240
cagacccttc aagcagcctg gctggggccc aggactgagt ctggggtcag ctttcacggt 300
cgcttttccc ttcgtcacca cccaccacag cccaccttgc atgcatggcc agcccctcca 360
ctccagcctg agccatgtgt gcccctgogg gaggacccat tcatgccaga aagctggtaa 420
ctccctccca gcatccctgc ggaaggagtc agtttctgag agtgtgactt ttcaaggcga 480
atgatgggga aggggtcccc agtccccaca gtggccccac ctctggggcc tgcaccagag 540
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gcactgcagt atattcttgc caaagatttc ctttaaaagc aagcactttt actaattatt 660
attttgtaaa tgtttatctt cttctgtctt ctcctccctt gaatctattt tactgttgtt 720
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gtattgtaca ctgacgcgtc cccactcctg tacagctgct ttgtttcttt gcaatgcatt 2460
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```

(2) INFORMATION ON SEQ ID NO. 26:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1668 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

gtatgccctc agaatcacga caactgttgc atgtaacatg gatctgtcta aataccccc 60
ggacacacag acatgcaagt tgcagctgga aactggggct atgatggaaa tgatgtggag 120
ttcacctggc tgagagggaa cgactctgtg cgtggactgg aacacctgcg gcttgctcag 180
tacaccatag agcgggtatt caccttagtc accagatcgc agcaggagac aggaaattac 240
actagattgg tcttacagtt tgagcttcgg aggaatgttc tgtatttcac tttggaaacc 300
tacgttcctt ccactttcct ggtggtgttg tcttgggttt cattttggat ctctctcgat 360
tcagtccttg caagaacctg cattggggac aacaaaggaa gtagaagaag tcagtattac 420

taatatcatc aacagctcca tctccagctt taaacggaag atcagctttg ccagcattga 480
aatttcacgc gacaacgttg actacagtga cttgacaatg aaaaccagcg acaagttcaa 540
gtttgtcttc cgagaaaaga tgggcaggat tggttgattat ttcacaattc aaaaccccag 600
taatgttgat cactattcca aactactggt tcttttgatt tttatgctag ccaatgtatt 660
ttactgggca tactacatgt atttttgagt caatgttaaa tttcttgcat gccataggtc 720
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ttgactcaga gagtcgctgt ccagtcctgtc attgctgcta ctctaaca 1668

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09645569.092000

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1768 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260" 69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

ctccgagggc aggaacgctc cgtctggaac ggcgcagact tttgccatgg gcttcatgac 60
gggcaccatt tccagtatgt accaaaccaa agccgtcatc attgcaatga tcactactgc 120
ggtaggtatcc atttcagtca ccatcttctg ctttcagacc aaggtggact tcacctcgtg 180
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cttcaccttt gtgctgcagc tgatggggga tcgcaattaa ggagcaagcc cccattttca 480
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gaaatcaaat cagcccaagg atatagttag gattaattac ttaatagaga aatcctaact 1680
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aaaaaaaaa gtaaaattaa tttgtgtt 1768

```

0954559.092000

(2) INFORMATION ON SEQ ID NO. 29:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3479 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000260" 69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

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aacaagaaac attttacaac cagtctgggc tcacttttgc attttttatg catgtctggg 3360
gcacaagctt tgaaaactac agcaaacagt aataaatgtg actgttttgt agttataaga 3420
gagaaaaaaa agaaaaaaga ggaaaaaaa agaaagaaaa aagaagagga ggagagaac 3479

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(2) INFORMATION ON SEQ ID NO. 30:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 933 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

gctcctccct	tccttctttt	tacatttttag	tcttagcatt	tactttcccc	acccacatt	60
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ttcatgaaaag	ggctgttaga	gctgcctggg	aagaaggcgt	gccttgggga	actgggaaga	180
tgccgtcagt	gtgggtgggc	aggaggacag	ccagtcgtcc	tgctgccagc	ccaatagctt	240
ccagcggcag	gtgcccagg	gctaccggag	cccctcatag	gggtaggggc	agggactgca	300
cctcctccag	gcactcatcg	taagcctcct	ggtactcctc	atggggcttg	accattatca	360
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gctgtttgga	aaaaagctgt	acaacctgta	tgccaggaag	tcaccaactg	atgaccacc	480
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aattggttgc	catcatttta	actcaatcag	actttgaagg	catggtccag	ccacacaggg	600
cctacattcc	cacatggcaa	ctatgaaagg	gtccagccc	agcaggggct	gtcccggctc	660
ctgccacccc	cacttctctgt	gcctcagatc	tgcccctgt	tacgtaagat	aaggacagct	720
acaggtccct	ctgagcctaa	acccacctaa	ccggactaac	atgggtgaag	atcttagctt	780
acaaagctct	ttcacatata	tctatctctt	tattctcata	gtccacagat	aactgactat	840
ttggttctta	ccatcaggcc	aaacggtaag	ttccttcaga	acagggcctc	ctgctttatc	900
ccaagaagtg	ataatgtagg	taccacaagt	cca			933

(2) INFORMATION ON SEQ ID NO. 31:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2783 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

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gacttttaaaa	aaattttttac	agttatttttt	atttttgtaga	atgagctgaa	agccagtggt	60
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tgcatacccc	atcaggaagg	ggaaaagatt	tctgcaaattg	agaatagcct	ggcagtcctg	180
tccacccctg	ccgaagatga	ctcccgtgac	tcccaggtta	agagttaggt	tcaacagcct	240
gtccatccca	agccactaag	tccagattcc	agagcctcca	gtctttctga	aagttctcct	300
cccaaagcaa	tgaagaagtt	tcaggcacct	gcaagagaga	cctgcgtgga	atgtcagaag	360
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ttaatttttt	agtattttacc	tgttaaagaga	ttatttagtc	tttaaatttt	ttaggttaat	1980
tttcttgctg	tgatatatat	gaggaattta	ctactttatg	tcttgccttc	taaactacat	2040
cctgaactcg	acgtcctgag	gtataatata	acagagcact	ttttgaggca	attgaaaaac	2100
caacctacac	tcttcggtgc	ttatagagat	ctgtgtcttc	ccaaataagc	ttttgtatct	2160
gccagtgaat	ttactgtact	ccaaatgatt	gctttctttt	ctggtgatat	ctgtgcttct	2220
cataattact	gaaagctgca	atatttttagt	aataccttcg	ggatcactgt	ccccctctt	2280
ccgtgttaga	gcaaagtga	gagttttaaag	gaggaagaag	aaagaactgt	cttacaccac	2340

```

ttgagctcag acctctaaac cctgtatttc ccttatgatg tccccctttt gagacactaa2400
tttttaaata cttactagct ctgaaatata ttgattttta tcacagtatt ctcaggggtga2460
aattaaacca actataggcc tttttcttgg gatgattttc tagtcttaag gtttggggac2520
attataaact tgagtacatt tgttgtacac agttgatatt ccaaattgta tggatgggag2580
ggagagggtgt ctttaagctgt aggcctttct ttgtactgca tttatagaga tttagcttta2640
atatttttta gagatgtaaa acattctgct ttcttagtct tacctagtct gaaacatttt2700
tattcaataa agattttaat taaaatttga aaaaaaagga aaggggaggg ggggtggagg2760
aaaaaaaaa gggcgggccgc cgc                                     2783

```

(2) INFORMATION ON SEQ ID NO. 32:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3411 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

gaagctctgt tgtctcggga acatgtcttg gaattggaga acagcaaggg cccagcctg 60
gcctcttttag agggggaaga agataagggg aagagcagct catcccaggt ggtggggcca 120
gtgcaggagg aagagtatgt agcagagaag ttgccaagta ggttcacga gtcggctcac 180
acagagctgg caaaggacga tgcggcgcca gcacccccag tcgcagacgc caaagcccag 240
gatagaggtg tcgagggaga actgggcaat gaggagagct tggatagaaa tgaggagggc 300
ttggatagaa atgaggaggg cttggataga aatgaggaga gcttggatag aaatgaggag 360
ggcttgata gaaatgagga gattaagcgg gctgccttcc agataatctc ccaagtgatc 420
tcagaagcaa ccgaacaggt gctggccacc acggttggca aggttgcagg tcgtgtgtgt 480
caggccagtc agctccaagg gcagaaggaa gagagctgtg tcccagttca ccagaaaact 540
gtcttggggc cagacactgc ggacctgcca cagcagaggc agctgttgcc ccgccggatg 600
ctggcctccc cttgccaggc ctaccagcag agggctcacc accaccaaag acctacgtga 660
gctgcctgaa gagccttctg tccagcccca ccaaggacag taagccaaat atctctgcac 720
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gggcaggcat cctggtggaa gatgccacct gtgtcacctg catgtcagac agcagccaaa 840
gtgtcccttt ggtggcttct ccaggacact gctcagattc tttcagcact tcagggcttg 900
aagactcttg cacagagacc agctcgagcc ccagggacaa ggccatcacc ccgccactgc 960
cagaaaagta tgtgcccttc agcaatgggg tgetgaaggg ggagttgtca gacttggggg 1020
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agttttcacc ggaagcagat gccgccatga gcgagatgac ggggaatata gcactgctg 1920
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tgatatttaa ccagttttta taaacttcat ttaggtctct aaacacagac tttttaaatt 2580
gcaactgtaa atatgaaatg gtcatcacat ctgacctggg tcagtgggga ggggaactgg 2640
tacctgcca agcctggttg taatttgtaa ccattttcta tttgtgcaaa ctctgtaa 2700
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caactgtaaa tatgaaatgg tcatcacatc tgaccttgg cagtggggag ggaactgggt 3060
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tgtgttttaa caaatgtaat attttgtaac agatacactg gagaacaaag ggaactcaa 3180
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agagactgtg atctgggaac tttttgctgt acaaaaagta actcattgaa ttaacttgca 3360
gtggtgtgtt tgattctttt ttagactggc ttcagcattg tgcagtttaa a 3411

```


(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1393 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

gaagaagaga aaaaagaggt gatgcttcag aatggagaga cccccaagga cctgaatgat 60
gagaaacaga agaaaaatat taaacaacgt ttcattgtta acattgcaga tgggtggttt 120
actgagttgc actccctttg gcagaatgaa gagcgggcag ccacagttac caagaagact 180
tatgagatct ggcacgcagc gcacgactac tggctgctag ccggcattat aaaccatggc 240
tatgcccggt ggcaagacat ccagaatgac ccacgctatg ccatcctcaa tgagcctttc 300
aagggtgaaa tgaaccgtgg caatttctta gagatcaaga ataaatttct agctcgaagg 360
tttaagctct tagaacaagc tctggtgatt gaggaacagc tgcgcggggc tgcttacttg 420
aacatgtcag aagacccttc tcacccttcc atggccctca acaccgcgtt tgctgaggtg 480
gagtgtttgg cggaaagtca tcagcacctg tccaaggagt caatggcagg aaacaagcca 540
gccaatgcag tcctgcacaa agttctgaaa cagctggaag aactgctgag tgacatgaaa 600
gctgatgtga ctgcactccc agctaccatt gcccgaaatc cccagttgct tgtgaggtta 660
cagatgtcag agcgtaacat tctcagccgc ctggcaaacc gggcaccgga acctacccca 720
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gaccttcctc actttctctt gtcccagctt ctcccctggg ggctgagag accctcacct 840
tccttctgcc catcttccat gttgtaaagg aacagcccca gtgcactggg ggaggggagg 900
gagtgagggg cagtgggtgcc ctccctgcag aagagacatg cagcagtagc gctggcgcca 960
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caggaaccca gcggctctag ccactgagcg gctaaatgaa ataaagtgga aaaaaaaaaa 1260
aaggaaaaaa ccaaaagcat aaaaaaccac agcaaatttc ttgatgaaaa ttgaaaataa 1320
aagtttcctt gtatttttaa aagggaaaaa gaaggaaaaa aaggagaggg aaaaaggagg 1380
gggggagagg agt                                     1393

```

(2) INFORMATION ON SEQ ID NO. 34:

000260"69594960

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```

gtgggccacc cctaactact attgcttctt aaaggtatct tcaccctctt cgcctgggtac 60
agccctcaca gctcttcaga gcaagcactg gactacaagg gcatgggtca caaaagggtta 120
atggatgggg gttacctagc cctggctaata tccccttcca ttcccaactc tctctctctt 180
tttgaagaaa aatgctaagg gcagccctgc ctgccctccc catccccgcg tgtaaataata 240
cactatcttt gatagcacac atggggcccc catatctctt ggccttggtt ttgatgttga 300
aatcctggcc ttgggagaga tgccttcag gcagacacag ctgtctgggt caggccaagc 360
ccctttgcaa tgcaagccct ttctgggtgt atgaagtccc tctatgtcgt cgttttcacc 420
agcaactggt gactgtccct tcgacacgga cctgctttga gatttcctga cagggaaaag 480
atctctgtcc atttttttcc tgtgcctaac agcataattg ccttttccta tgtaaataat 540
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aaagccatta ttctctgatg cactgtttgc ccagtaact cactttaaaa cctctctttc 660
cagtgttccc tctctccctc cagggccact gcttgaagaa gaatatgtat gtttctatct 720
tgtatgtctg tgtgcccctc ctgccccgaa agtgctgact atgggggaaat cttttagctg 780
ctgtttttag actccaagga gtggaaatta tgtggaagaa gcaaacctga tacaatttgc 840
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atctctacat gttttagaca gagacaattt aaggcctgca ctcttatttc actaaagaaa 1080
aactaatgtc agcacatgtt gctaatagca gtggattttt ttttaataaa aaaagtttac 1140
agatcaaatg tgaaataaat atgaatggag tggctcctct gtctgttatc tgagttttcal 1200
aaagctttta gactctggga acatctgatt ttatgg 1236

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000260"69594960

(2) INFORMATION ON SEQ ID NO. 35:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 749 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

ggagatgcag aggtaaaagt gtgagcagtg agtttacttt tcaaggcatc ttagcttcta 60
ttatagccac atccctttga aacaagataa ctgagaattht aaaaataaaa aaatacataa 120
gaccataaca gccaacaggt ggcaggacca ggactatagc ccaggctctc tgatacccag 180
agcattacgt gagccaggta atgagggact ggaaccaggg agaccgagcg ctttctggaa 240
aagaggagtt tggaggtaga gtttgaagga ggtgagggat gtgaattgcc tgcagagaga 300
agcctgtttt gttggaaggt ttggtgtgtg gagatgcaga ggtaaaagtg tgagcagtga 360
gttacagcga gaggcagaga aagaagagac agggaggaaa gggccatgct gaagggacct 420
tgaagggtaa agaagtttga tattaaagga gttaagagta gcaagttcta gagaagaggc 480
tggtgctgtg gccagggtga gagctgctct ggaaaatgtg acccagatcc tcacaaccac 540
ctaatacaggc tgaggtgtct taagcctttt gctcacaaaa cctggcacia tggctaattc 600
ccagagtgtg aaacttccta agtataaatg gttgtctgtt tttgtaactt aaaaaaaaaa 660
aaaaaagttt ggccgggtgc ggtggctcac gcctgtaatc ccagcacttt gggaggccaa 720
ggtgggggga tcacaaggta actagatgg
749

```

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

09646569 "092000

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gtgaccccca taggcctgag gcttgtgcag gcagtgggcg tggggtaagg cttcctgatg 60
ccccctgtcc ctgcccagaa cctgatggcc ctcatatgct cttggctctt atcttggaag 120
cacaggcgct gacagccgtc ccagcccttc tgtctgcggg cctgaaccaa acggtgccat 180
ggggaactgt ctgcacaggg cggagtctcc ccctcaactg agaactcaag tcagctggac 240
ttcgaagatg tatggaattc ttcctatggt gtgaatgatt ccttcccaga tggagactat 300
gatgccaaac tggaagcagc tgccccctgc cactcctgta acctgctgga tgactctgca 360
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atgcttttca gacctctctt ccgctggcag ctctgccctg gctggcctgt cctggcacag 480
ctggctgtgg gcagtgcctt cttcagcatt gtgggtgccc tcttgcccc agggctaggt 540
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gagctgaagg ctttgcaggc cacacacact gtagcctgtc ttgccatctt tgtcttgttg 840
ccattgggtt tgtttggagc caaggggctg aagaaggcat tgggtatggg gccaggcccc 900
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ctgctcctcg ccctattctg ccaccaggcc acccgacccc tcttgccctc tctgcccctc1140
cctgaaggat ggtcttctca tctggacacc cttggaagca aatcctagtt ctcttcccac1200
ctgtcaacct gaattaaagt ctacactgcc tttgtgaaaa aaaaaaaaaa a 1251

```

(2) INFORMATION ON SEQ ID NO. 37:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 3283 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

000269" 6554550

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

ctggcctcag caccttccag aactgggttac ctagtaccce cgccacctcc tgggggtggac 60
tcaccagttc caggaccaca gacaatggtg gggagcagac tgccctgagc ccccaagagg 120
ccccgttctc tggcatctcc acgcccccg atgtgctcag ttagggccc gagcctgcct 180
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000260 "69594960

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 gccctagacc tttggggctg cagctggctg agcgccgagg ggctgcggag gcagtgacct1140
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 agcgtgcctt gcccctctcg gagcctgggg tcaactcagac caccagccaa gaggccttcccc1260
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 aagggcctct gtttgccccg ctagcaaccc ttttatatct agcagggtct tccagtcct1380
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 ccaaggcagg ctgctactgc ctttgctgac ccccggggtg gcctcacggt ggggacaaag1620
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 agccttctcc tcagcccagc acccatggcc atcgaggct aggatgccag acacagccat2460
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 ggctacgctg ggcaggacga caaacacgag acgccactgt ggaatgagca acttcggagc2640
 acgggggtgac ttgcttggga ccgtgcccac gtgacagccc cttatgcaga ggaggaaa2700
 gaagccccga gtgggagggg aacctgtcca aagtacacg gtgtgtgggt gacacagctg2760
 ggggtgagtc aggtcggccc ctgaggccca tgctccctga acgctggaga ccactgtcgg2820
 ctagcagcgg ctctcaggga aggcctggtc tccacctcc cagcctagcc tcgcgagccc2880
 tcgtcctccc cacatcggac ctgctcacct gcctggaccc tgggctgcca gatgcaggaa2940
 gcatcaaacc cccagcctc gtgggtgcgg ggcaggggcg aggcagcaca gcttagatgc3000
 cctggtttgt cctcttctgc tcttggaag agcttgctcc cgcccagctc tctgccact3060
 ggcttttcag ggttgggctg ggcccagag gccttttagt cgcttctcac ggtggcctga3120
 tggctcaacc cagtcccaaa cgggcccagt gacactgccg actgcacccc agctcaggcc3180
 cccactgcac cagcaatgct agaaaaccaa gccataaaaa gtgatttctt ttttcattaa3240
 aaaaaagaaa aaaagagaca gaggaagtag atgctggccg ggc 3283

(2) INFORMATION ON SEQ ID NO. 38:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2720 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

gaggggagaa ggaaqqaaqq

2720

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

gccggccgcc ctttttaacc cccttccctt cctttttttc tgttgctgaa tgatatttta 60
ttagcttgat aatttgggcc tgcccttagc attaataagc ttcagcacta gtcacaagac 120
tttcattcac tgggtggggaa actttcttgt tttaaaaaat gcaattcaag aaagggcatc 180
tatttcttgg gggctgcggt gacagcaggc ttctcttcac gggtgatggg aatgggtgcgc 240
tcagggccag agacctgttt ccttggtcca ttcacagtga ggacccccatc agatgacagg 300
gatgaagtaa tggtgagagg gtctacatca gctgggateg ggtatttccct gtggaactcc 360
ctggagatga aaccatgttc atcctggcgc tcttcagtgt ttccatgcac ctcaatcaca 420
tctcccaaca ccttaacttt gagttcctct ggggagaagt gcttcacatc caggttgaca 480
gagaacctgt ccttctccag gcgcctctct gagagtcagg tgtcaaacca gctgggtgcc 540
cgcaggaagg aggggtggcg aaggtagaag ggactcaggg aagtagacgt cgggaaaaga 600
tcagactcca acaggtgctc tccgaagaac tgggtcaaaga ggcggctggg ggagtggaaa 660
ggaaagaagg ggcggcggt ccaggggtgg tggatggcga tgtccatggt ggctaggtga 720
gtgtgagggg tcagctggcc tggtcagctc cttcagctgc agctacagcc agccccttat 780
atatgcagtc ttgtgaagct tctggaatgg tgatgtcagg ggttttatta tcctagctca 840
ccagcagttc atggagactt gtgatccggg atttggaat gtgacacata cccagtactc 900
actgagctaa gaaaagagag acacaaacac gtctgagccg gccagtgact tgtcatggtc 960
ttgtttcact agctttctgt ccacacccaa tggcaccac cccaccctt gttctctgaa 1020
gctggtacag agtcag                                     1036

```

(2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2659 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

00646569-092000

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

accacacggg ctgccctccc ctgcgcactc ccctcgctgc ccgggccccg agcgcagtgg 60
ggccgcacag attcacaatg ttgaaagccc ttttcctaac tatgctgact ctggcgctgg 120
tcaagtcaca ggacaccgaa gaaaccatca cgtacacgca atgcactgac ggatattgag 180
gggatcctgt gagacagcaa tgcaaagata ttgatgaatg tgacattgtc ccagacgctt 240
gtaaagggtg aatgaagtgt gtcaaccact atggaggata cctctgcctt ccgaaaacag 300
cccagattat tgtcaataat gaacagcctc agcaggaaac acaaccagca gaaggaacct 360
caggggcaac caccggggtt gtagctggca gcagcatggc aaccagtgga gtgttgccc 420
ggggtggttt tgtggccagt gctgctgcag tcgcaggccc tgaaatgcag actggccgaa 480
ataactttgt catccggcgg aaccagctg accctcagcg cattccctcc aacccttccc 540
accgtatcca gtgtgcagca ggctacgagc aaagtgaaca caacgtgtgc caagacatag 600
acgagtgcac tgcagggacg cacaactgta gagcagacca agtgtgcatc aatttacggg 660
gatcctttgc atgtcagtgc cctcctggat atcagaagcg aggggagcag tgcgtagaca 720
tagatgaatg taccatccct ccatattgcc accaaagatg cgtgaatata ccaggctcat 780
tttattgcca gtgcagtccct gggtttcaat tggcagcaaa caactatacc tgcgtagata 840
taaataaatg tgatgccagc aatcaatgtg ctacagcagt ctacaacatt ctgtgttcat 900
tcctctgtca gtgcaatcaa ggatattgag taagcagtga caggctcaac tgtgaagaca 960
ttgatgaatg cagaacctca agctacctgt gtcaatatca atgtgtcaat gaacctggga1020
aattctcatg tatgtgcccc cagggatacc aagtggtaga aagtagaaca tgtcaagata1080
taaataagtg tgagaccaca aatgaatgcc gggaggatga aatgtgttgg aattatcatg1140
gcggtcttcc ttgttatcca cgaaatcctt gtcaagatcc ctacattcta acaccagaga1200
accgatgtgt ttgcccagtc tcaaatagcca tgtgccgaga actgccccag tcaatagtct1260
acaaatacat gagcatccga tctgataggt ctgtgccatc agacatcttc cagatacagg1320
ccacaactat ttatgccaac accatcaata cttttcggat taaatctgga aatgaaaatg1380
gagagttcta cctacgacaa acaagtccctg taagtgcagt gcttgtgtct gtgaagtc1440
tatcaggacc aagagaacat atcgtggacc tggagatgct gacagtcagc agtataggga1500
ccttccgcac aagctctgtg ttaagattga caataatagt ggggccattt tcattttagt1560
cttttctaag agteaaccac aggcatttaa gtcagccaaa gaatatgttt accttaaagc1620
actattttat ttatagatat atctagtgtc tctacatctc tatactgtac actcaccat1680
aattcaaaca attacacat ggtataaagt gggcatttaa tatgtaaaga ttcaaagt1740
gtctttatta ctatatgtaa attagacatt aatccactaa actggtcttc ttcaagagag1800
ctaagtatac actatctggt gaaacttgga ttctttccta taaaagtggg accaagcaat1860
gatgatcttc tgtggtgctt aaggaaactt actagagctc cactaacagt ctcataagg1920
ggcagccatc ataaccattg aatagcatgc aagggttaaga atgagttttt aactgctttg1980
taagaaaatg gaaaagggtc ataaagatat atttcttttag aaaatgggga tctgccatat2040
ttgtgttggg ttttattttc atatccagcc taaagggtgg tgtttattat atagtaataa2100

atcattgctg tacaatatgc tgggtttctgt aggggtatttt taattttgtc agaaatttta2160
gattgtgaat attttgtaaa aaacagtaag caaaattttc cagaattccc aaaatgaacc2220
agatatcccc tagaaaatta tactattgag aaatctatgg ggaggatatg agaaaataaa2280
ttccttctaa accacattgg aactgacctg aagaagcaaa ctcggaataa ataataacat2340
ccctgaattc aggacttcca caagatgcag aacaaaatgg ataaaaggta tttcactgga2400
gaagttttta tttctaagta aaatttaaat cctaacactt cactaattta taactaaaat2460
ttctcatctt cgtacttgat gctcacagag gaagaaaatg atgatggttt ttattcctgg2520
catccagagt gacagtgaac ttaagcaaat taccctccta cccaattcta tgggaatattt2580
tatacgtctc cttgttttaa atgtcactgc tttactttga tgtatcatat ttttaataaa2640
aaataaatat tccttttaga

```

2659

09646569 "092000

(2) INFORMATION ON SEQ ID NO. 41:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2939 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00250" 59594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

tttttttttt ttttttttgt ggtaataaaa tgttgtcaat tttattaaaa gctgattcca 60
tttcttcaca cagttaagta cgtttctttc ttgttttgtt aaagccatt tcataagagt 120
gagttggctc tgtgagacca tcttgataa agacacatac agttagcacc acacatttat 180
aaatgcagat agccacaatg acctttccaa tatgtacaag ctccatttac acatccacac 240
atgtatttac agctaataaa taaaatgtaa agccagaaca tccttgatat atataacaaa 300
gtttttcgga gccagagttc ccagtgtctat gtgctgtctt agtgaatctt ttaagttaat 360
gcacctggg tcacaaccca aatccagaaa tttaatgaat taataaaggg gatgccaaca 420
acaaatcata catcatttta ttttagaga gaattcattc caagcctgat gatgttaatc 480
acaacattgg tcctactatt tataggcacg atcatctctc tcagagaaag ggtcgaagtt 540
ctggcacatc aggaacaatt tctactccga catgttccaa tacatccctt gatcgactgt 600
tttcccttcc gaattatgct gaaggacaac acacatgcag agctttctag tatgtgttca 660
gatatcacat actttcacag tcgggttccc agctatagcc tctgagatat ttgacatctt 720
tatcatttca tatttatacg tagaagagca ttctgaaaaa taggagatct agtttataaa 780
tagttgttca ctcaactctg attagttgtt aaaaacaaca aatagcaacc ctcatggtac 840
tccatctggc tcattgcacg cgatggttta caagcactgc ttaggaatcc accccaggaa 900
cctctccacc cttttactta gtaaaaacgg tccttgtcta aaatctgtag aagctcacac 960
aatgcaaaat ttgaactcaa acctatcttt tcatgtcaaa gccaggaaca aaagagacgc 1020

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actggaagta caactgaagc atgaccaagg taagcctaaa actgaagagt aactgtcaga 1080
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tctttttttt tttctgcacc attcaaatta tgtgtcagct gaggattaca ggctcatttt 1200
caacacctac ccagagaaca ttattataat ataactctga gacaaaaaag aagggggaga 1260
gagggattaa gcaataaacg ataaagccta ttaagaatta attgatctag attttatatc 1320
tccttgaaat tgtaactttg tcatgatgca ggccaatggt agggactgtt taaaacctct 1380
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accacattcc aatagcaaga gggaatcatt ctataactg attcactctg ctgtgtagat 1500
gagtctgatt cgtgccgcgg aaaagcattt tctgtattct tggagactta gagtaaagtt 1560
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tataggctat ggccaatac gccacatgaa ggagccttat tttactctgc gctcaaacaa 1680
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aggtgtgct atttggccac tatacccat aaattgaatt agccactttt tagtgcttga 1800
gactgtctcc taaaataact aacaagggta gggctgggat taatattcag gaaaatccac 1860
ttttgaaaca ccccaaacac tgggtatggt ttgtaaaagt tacttctctc acttcattct 1920
tcacagaatt cacatgccgt tctttgttct gtagattcgc ccagtttcag cctgacttct 1980
tattcagaga cttgtcatgg catttcacaa ataccgcagg tgcttttctt ttctgcaaat 2040
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tgatcttctg aatggcgaag ccgggactgc tccaccagtc tgaccagcta aagtatgaat 2160
cactcttcca tttgagcttc aacatgagta gttctccaat atctacctct gtgtaaatta 2220
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atgtgtgtaa gacgtctaca aaatctgcat catcaggaga aagacgactc ggggcttctg 2820
catactcaaa gttaggcca gctggatcga ggccagtaat tctgttgaac tttcttattg 2880
gtcagacttc ctgcaatgcc agcagcatgg gctccaaggc tgtatcccaa gagatggac 2939

```

000250" 69594960

(2) INFORMATION ON SEQ ID NO. 42:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3670 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

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gcatcgccat gacgcccgcc aatgccaccg aagcctccaa gcccgaaggc acaacgggtgt 60
gtcctccctg tgacaacgag ttgaaatctg aggccatcat tgaacatctc tgtgccagcg 120
agtttgactt gaggatgaaa ataaaagaag tgaaaaaaga aaatggcgac aagaagattg 180
tccccaaaga gaagaagccc ctgaagttgg ggcccatcaa gaagaaggac ctgaagaagc 240
ttgtgctgta cctgaagaat ggggctgact gtccctgcca ccagctggac aacctcagcc 300
accacttctt catcatgggc cgcaagggtga agagccagta cttgctgacg gccatccaca 360
agtgggacaa gaaaaacaag gagttcaaaa acttcatgaa gaaaatgaaa aacctatgag 420
gccccacctt tcagtccgtg tttaagtgat tctcccgagg gcagggtggg gagggagcct 480
cgggtggggg gggagcgggg gggacagtgc cccgggaacc cgggtgggtc cacacacgca 540
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ccatttagat taggaagggt tttaagatcc gcaatgtgga gcagcagcca ctgcacagga 720
ggaggtgaca aaccatttcc aacagcaaca cagccactaa aacacaaaaa gggggattgg 780
gcggaaagtg agagccagca gcaaaaacta cattttgcaa cttgttggtg tggatctatt 840
ggctgatcta tgcctttcaa ctgaaaaatt ctaatgattg gcaagtcacg ttgttttcag 900
gtccagagta gtttctttct gtctgcttta aatggaaaca gactcatacc acacttaca 960
ttaagggtcaa gccagaaaag tgataagtgc agggaggaaa agtgcaagtc cattatgtaa 1020
tagtgacagc aaagggacca ggggagaggc attgccttct ctgcccacag tctttccgtg 1080
tgattgtctt tgaatctgaa tcagccagtc tcagatgcc caaagtctcg gttcctatga 1140
gcccggggca tgatctgatc cccaagacat gtggaggggc agcctgtgcc tgcctttgtg 1200

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09646569.092000

tcagaaaaag gaaaccacag tgagcctgag agagacggcg attttcgggc tgagaaggca1260
 gtagttttca aaacacatag ttaaaaaaga aacaaatgaa aaaaatttta gaacagtcca1320
 gcaaattgct agtcagggtg aattgtgaaa ttgggtgaa agcttaggat tctaattctca1380
 tgttttttcc ttttcacatt tttaaaagaa caatgacaaa caccactta tttttcaagg1440
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 tccgaggctg cttcccagag gagcagctct ccccgagcat ttgccaaggg aggcggattt1560
 cccctgtagt gtagctgtgt ggctttcctt cctgaagagt ccgtggttgc cctagaacct1620
 aacacccctt agcaaaactc acagagcttt ccgttttttt ctttctgtta aagaaacatt1680
 tcctttgaac ttgattgcct atggatcaaa gaaattcaga acagcctgcc tgtccccccg1740
 cactttttac atatatattgt ttcattttctg cagatggaaa gttgacatgg gtggggtgtc1800
 cccatccagc gagagagttt caaaagcaaa acatctctgc agtttttccc aagtaacctg1860
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 ggggccctag cctgacccgg aggaaaggat ggtagattct gtttaactct gaagactcca2160
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 tgtgaaaatg ttttacattc catttcattt gtgttgtttt ttttaactgca ttttaccaga3540
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 aaaaaaaaaa

3670

092000 "092000" 092000

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1025 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

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ctttaaccag ttatttacag tgtgctcatt cgttcagaaa ttagatacaa aatctcaaga 60
cctgttacta ctgattttat taaatcagag tctttaattc ttgcatgttt gtatctaatt 120
tctgaacgaa tgagcacact ttaaccagtt atttacagtt acctttttcc ttttaaccgga 180
ttgtgaaagc ttcatgtatt ttaatttaga ttctgtgttt ttaaggggtc tgagcatgaa 240
gctggcagat agtcggcagg actcattttt tcatcatggc tggctgattt ctccatagat 300
tgataacagt attttgttat cttgcttctc tgtagttttg catcagctgt ttaactttga 360
gctgagttag gggagagggg taaagagaaa gaaacttaag ttttctttca cagaactcca 420
ccattgtggg ctttgagaga gccctaaagc attgtacctt gtggtacctt gtgacttcca 480
accaaagcct ttgagtatgc actaaatagg tgagaagaaa ggagagaagg tttttagggt 540
agaaaccttt aaccgataga aggatatggt atgttgtaaa gctggaacca agtttgcatt 600
tttgagggct tgagatgaag ggaagactct taccagatag taagacagct gagttttcct 660
cagttttctc gtcttaacac tagtggacaa ttctagcatt ttgtttgagg gatttcagag 720
ttaacctcat ggaattcagg attttttagc aagtttgctt ttggttttat cttggctttt 780
agtaatcatg ttggctggtc tggtcacagg tgactgtgaa acagatgccc tggctctgct 840
ttcatcactc taggatcatg aagtgcctat ctatttcctg gttatgaata ttaagggttg 900
aattacattt ttattgattg tttggatcag agctcagttc ctgtagaaaa cgaactgtaa 960
aagaccatgc aagaggcaaa ataaaacttg aagtgaatgc taaaaaaaaa aaaaaaaaaa 1020
aaaaa                                           1025

```

(2) INFORMATION ON SEQ ID NO. 45:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 538 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

000260 " 6954960

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

gccacggggtc cggccacggg tgccggccacg ggtccgacaa tagtatgcag ctaaaaaata 60
attgtatgtc tttatatact aatatgtaat aatcttcagg tgaaaaaggc aagccacaga 120
aatgtgtata gcgcacttcc catttggtgt tcagaaagga gtagaatata aacacataat 180
tgcttatgta tgcttattca gaataaatgg gtaacactga ttacttttgg gaggggaacc 240
agtaggttga ggacaggaga gggaagggtc ttaacactta caccctttg tacattttga 300
atthtgaacc atgtgactgt attacctatt caaaataaac aataaatggg cccaaacagg 360

```

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2192 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000250" 69994960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

gaggcctgcg cccacaccct ctccctgtcca gccctcgccc gcctgggcag ggcccggcgc 60
cgtccgtgga tgagccacag aacctcttcc accttccgag cggagagaag ttccattcc 120
tcttctctt cctcctccgc tgccacctcc tctcggcct cccgtgctct cccggcccag 180
gacccgccc tggagaaggc cctgagcatg ttttccgatg actttggcag cttcatgagg 240
ccccactcgg agccccctggc cttcccagcc cgccccggcg gggcaggcaa catcaagacc 300
ctaggagacg cctatgagtt tgcggtggac gtgagagact tctcacctga agacatcatt 360

gtcaccacct ccaacaacca catcgagggtg cgggctgaga agctggcggc tgacggcacc 420
gtcatgaaca ccttcgctca caagtgccag ctgcccggagg acgtggaccc gacgtcggtg 480
acctcggtc tgcgggagga cggcagcctc actatccggg cacggcgta cccgcataca 540
gaacacgtcc agcagacctt ccggacggag atcaaaatct gagtgcctct cccttccctt 600
tccctgtgcc ccccgcccca cgccctgccag caaagcctcg ctaaccccat tacaacagct 660
ccaggacatc tcagcccagg ttctagcccc cagcaccccc agaccccagg tggaccatcc 720
tcccaaacta gggccctcca ctctatccag ggcaggccag ggactccctg gcctgacaca 780
tgatgcccag atttcagatt tggcctccgt cacttaatcc agagtacagg ggctggggtc 840
agggaaaggaa gatctaaaga acccactgtg ggtcagggga atgggaccag caggacatat 900
gggcaagctc tgcaggacag acaggcagac aaaccctctg atctatgaag tctctgcagg 960
gcaaggggac cagggacctg gaaccctctt ggccaagggg agtgggagag acagagggaa 1020
ggtcacaggc aagggtgcct atctaagtgg aactaattgc ccgagggtc agcaagggca 1080
agaggagaca gccgtgacgg taaacttccc ctctaccagc ctccaagccc cagccagcg 1140
agcaggctgc ctgcccaccc cgtgccccca gccagctggc tgtgccaggg cagagccatg 1200
ccacatctgt atatagatgg ggtttttcca atacagctgg ttcgtgataa actgcatgaa 1260
actcctgccg tectgcgcct gctggggcct ccaggcaagg ccacgtgggg ttgggggtgg 1320
ggctggtcct tctccctccc acaggcctgt gttcttgggg ctgctcccat gcagacagg 1380
tcacctaaac gagatggaag ccagggcctg gatggggcct tgggtcctcg aggttgga 1440
ccagcttctt gccaccttcc cctccgggca gtcagctctc catccatccc cctctttaat 1500
ctatgaatct ataggctcgg tgtgtgtaac acacacaccc ctatcgttgt ccttcaaata 1560
ctcagcatta ccattggttg aggccaaatt cagagcttcc tcaaatcaga tttacaatct 1620
ccattttcat taacggggaa acatccccga gccactgagt gctgtgcttt gtcactgaag 1680
gttagatctg aaccaggggt gtcaacagct gctctcaact cccacacctt gggcactgag 1740
gagtatttcc cctcattcta cctctctaag gctatgcacc cctccccacg tcttcagct 1800
gggggatggg gggagtcata ggaaaagccc ccatctccca tctgggatag ggaccttcca 1860
tcagccttaa ccctgggaaa tgccctgtgc cccagtgac tcttggtttc gtctcccaca 1920
tacagaagca ggggtggagg gaagggtggg tctcagttag caggggtccc cagggcaagt 1980
cagcctctc cctccatgcc tctctggtca gtgtgcctta ggggtggcct tcaactccac 2040
cactctgggc cccttggggg aggactgggg agggggccgt gggagagccc tgacgctgga 2100
acctgtatcc acaataaagg acagtctcac agacaaaaag aggccgcctg ccggagttct 2160
caaaccttag gcagggcctt acttgagaga aa
2192

```

000260" 69594960

(2) INFORMATION ON SEQ ID NO. 49:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2952 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

gtgCGgatgc cggccggcag cagcatcatg gctcacgggc cggcgcgct gatgctcaag 60
tgcgtgggtg tggcgacgg ggcgggtggc aagacgtgcc tactcatgag ctatgccaac 120
gacgccttcc cggaggagta cgtgccacc gtcttcgacc actacgcagt cagcgtcacc 180
gtggggggca agcagtacct cctaggactc tatgacacgg ccggacagga agactatgac 240
cgtctgaggc ctttatctta cccaatgacc gatgtcttcc ttatatgctt ctcggtggtg 300
aatccagcct catttcaaaa tgtgaaagag gagtgggtac cggaacttaa ggaatacgca 360
ccaaatgtac cttttttatt aataggaact cagattgac tccgagatga ccccaaaact 420
ttagcaagac tgaatgatat gaaagaaaaa cctatatgtg tggacaagg acagaaacta 480
gcaaaagaga taggagcatg ctgctatgtg gaatgttcag ctttaaccca gaagggattg 540
aagactgttt ttgatgaggc tatcatagcc attttaactc caaagaaaca cactgtaaaa 600
aaaagaatag gatcaagatg tataaactgt tgtttaatta cgtgagaaac atcttcagt 660
gccaaggaaa ctgtccattt ctctcagaaa gcaaatgaaa tgctacagct ataccagac 720
cttttatagg taatgaagca gttcaaaact tgaaagaaaa caaacctgt cctcagaatt 780
ctataaagtg tattaagaat gttccttaaa ggtttaagaa gcagtaagca gcatctgaag 840
ccacaatcta ttataaatac tttatttcaa ctagaaggta caatctctca ggggtttcat 900
agttaaaaaa gctacaatca catcatgttg taactacgta aaaaacagag ctgtaaatgg 960
aactgcttgg ctttgaccat acacatttct gccagccct tacagaatct gcacaaagaa 1020
atatctccct ttgctccagt taattgttct tgtatgtaag ttgctttcta ttccagtata 1080
tccagagtg tgaataaca aggccagcca cgtagccaaa ggtcgctcca agcgtacagg 1140
agatgggcca tacttgagga gagaatgtat gagatcaaaa aagaacaaat gttttattat 1200
tacttgagca caagtgtaac ctaaatattt ctatattaaa gcttaatgtg ctttcttaaa 1260
gaatgccaaa agtgtataa ggtcataact gcatttatca tgaacactaa aaatgtacac 1320
attttagtta atgtgcatta aactgtaaca aggttcttg caattgtaga tttagttgag 1380
cgctcccaa agtgcagtag acacatgcta aaattacaaa taaaatttt gggtcagact 1440
ttgccataat gatagactca atttagctct ctgaactagt tggtaatttt ttttttttaa 1500
ttcccacttt ggctgtgtac atcaaatgaa atgagaagtg tgtatgctga ccaaaccaca 1560
agaaactttc ttaagtgtgt gttaaagagg aaagacctag aatccaagcg tgttacatga 1620
aaattgtaac agagcagctg ctccacctt tcagatatag atgttgaac cacagcagaal 1680
gttatagagc gacaacttat atacacacct agaattgaag ttaacaaaaa taccggctct 1740
cagagacccc ttttctccag ccatattaca tcaggctaga agtaattaat gttgatttat 1800
ttcatctaca agcagttggt cctaagtga aaggctctgc ttgaaaaaaa aaagaaaaaa 1860
aagttggagg aaaattttca tgttcttctg tgaagcttat ttggtacact ggagccattt 1920
ctaacttttc tctgggggga acaggccaca gaactgtgtt agaggtgaac catcttaatt 1980
actagttcta ttacctaat cagcttcctt gtttggtctg ctgtggatct gccttattgc 2040
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gaacaaccta atgcatttta gagaaacaat ctcatcacat ttttcttagc ctttcttaca 2160
tttaaacttg ctgttgccca aattataatt tttaaatgt ctttggtggg cttctgttaa 2220
ttcacatgac ttgagcttat agctatgtct actgcacaga ttgggtaatg gaacactaaa 2280
cttttatact tgaaaatgac agccttaaat gctcatatca gtcacaaatc taggatgtac 2340
tgtcttggtg tatgtgagct ttgtagagat ttttaaaaaa ataagcatca ccttccattt 2400
gaagagtggg gagagtctac tggatgactg gccaggaact ttctctctga atcggacatt 2460
tggatgtctt ctttcttcca agaaatggtg gttcacatta aagtatcatg gccttatgta 2520
tgctcaaatg gaactctatg taactttctt atttaatttt ggtctgctta ttttagata 2580
aaattgaaag gaattgtata aatcaattaa catattagct gagttgtcca acacatggta 2640
taaacgaatt acaacagtaa actattacac atttccaact tgcccttggg gatttatgag 2700
gatttttttt ggtgggggga gggggctcca attcatatct ctgaaacctt tcacacttgg 2760
tttactaatt caaagttaga agtctagaat ttgccctgcc ctaacagaaa cagatttagga 2820
atgtgtctac acaaactggg gtcacctgtt tcttgactgg gatttggttt cctcattata 2880
aatatgggag gtagaacaga gatctccaac gtctctccca tttatcacag taattttctt 2940
attcacagta at

```

09646569 "092000

(2) INFORMATION ON SEQ ID NO. 50:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 615 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

gcaaggatgg tctcaatctc gacctcgtga tccgccacc ttggcctccc aaagtgttgg      60
gattacaggc gtgactcacc atgccagcc acttagtttt ttcttattcc cacctttcta    120
tcccatagaa cactcttttt tatcttcctt gaaccatatt gatgagataa atagggctgg    180
gggctggggc ccgctgggtca ctcaacagag tatttccttt ggccgagatg gaagttttgt    240
cccaatagat gagctgctga gtatcaacaa ggtgacattt ttctgctgcc catttggtgc    300
ctggagacgg tggtagcctg aaggcagagg ccagctgccg caagacagca atgacagtcc    360
acctgccgac ctgattcctg catcatggaa taaccacatg gctaccttct atcctctgtt    420
cccaaattggt ggtggcactt atcctgaagt cgtcaatgat ttccctttga aactacttta    480
ttttactaat ttaaaactatt ttgtactgat gtagccctga ggtagttcat gaaaatgctg    540
tgcactcatt ccatggaata aatgttgga agctgatctt ttctgatata aaatgttgaa    600
tgataaaaaa aaaaaa

```

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

000260" 59594950

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

ttttactgac cttgctagaa gtttacagca aggaagtgca ggaacatttc acaaatctac 60
aatctgtgag tatcacatcc tgtatagctg taaacactgg aataaggaag ggctgatgac 120
tttcagaaga tgaaggtaag tagaaaccgt tgatgggact gagaaaccag agttaaaacc 180
tctttggagc ttctgaggac tcagctggaa ccaacgggca cagttggcaa caccatcatg 240
acatcacaac ctgttcccaa tgagaccatc atagtgtctc catcaaagt catcaacttc 300
tccaagcag agaaaccoga acccaccaac caggggcagg atagcctgaa gaaacatcta 360
cacgcagaaa tcaaagttat tgggactatc cagatcttgt gtggcatgat ggtattgagc 420
ttggggatca ttttggcatc tgettccttc tctccaaatt ttaccaagt gacttctaca 480
ctgttgaact ctgcttacct attcatagga cctttttttt ttatcatctc tggctctcta 540
tcaatcgcca cagagaaaag gttaaccaag cttttggtgc atagcagcct gggtggaagc 600
attctgagtg ctctgtctgc cctggtgggt ttcatatcc tgtctgtcaa acaggccacc 660
ttaaactctg cctcactgca gtgtgagttg gacaaaaata atataccaac aagaagttat 720
gtttcttact tttatcatga ttcactttat accacggact gctatacagc caaagccagt 780
ctggctggaa ctctctctct gatgctgatt tgcactctgc tgggaattctg cctagctgtg 840
ctcactgctg tgetgcggtg gaaacaggct tactctgact tccctggggg gagtgtgctg 900
gccggcttca cttaaccttg cctagtgtat cttatccctg cactgtgttg agtatgtcac 960
caagagtggg agaaggaaca accagccaat cacgagatac acatgggagg gcatttgcatt 1020
tgtgatggaa gacagagaag aaaagcagat ggcaattgag tagctgataa gctgaaaatt 1080
cactggatat gaaaatagtt aatcatgaga aatcaactga ttcaatcttc ctattttgtc 1140
agcgaaggga atgagactct gggaagttaa atgactggcc tggcattatg ctatgagttt 1200
gtgcctttgc tgaggacact agaacctggc ttgcctcctt tataagcaga aacaatttct 1260
gccacaacca ctagtctctt taatagtatt gacttggtta agggcattta cacacgtaac 1320
tggatccagt gaatgtctta tgctctgcat ttgccctgg tgatcttaaa attcgtttgc 1380
ctttttaaag ctatattaaa aatgtattgt tgaatcaaaa aaaaaaaggg agtgagaggt 1440
ggggtggggg gggggaggag ggggggcccgt ttaggggggg ccgggttt 1488

```

(2) INFORMATION ON SEQ ID NO. 53:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2262 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

09546559.092000

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

ctcgagccga ttcggctcga gctaattttt aagtctcgat tggaaatcag tgagtagggt 60
cataatgtgc atgacagaaa taagctttat agtgggtttac cttcatttag ctttggaagt 120
tttctttgcc ttagtttttg aagtaaatc tagtttgtag ttctcatttg taatgaacac 180
attaacgact agattaaaat attgccttca agattgttct tacttacaag acttgctcct 240
acttctatgc tgaattttga ccctggatag aatactataa ggttttgagt tagctggaaa 300
agtgatcaga ttaataaatg tatattggtg gttgaattta gcaaagaaat agagataatc 360
atgattatac ctttattttt acaggaagag atgatgtaac tagagtatgt gtctacagga 420
gtaataaatg tttccaaaga gtatttttta aaggaacaaa acgagcatga attaactctt 480
caatataagc tatgaagtaa tagttggttg tgaattaaag tggcaccagc tagcacctct 540
gtgttttaag ggtctttcaa tgtttctaga ataagccctt attttcaagg gttcataaca 600
ggcataaaat ctcttctcct ggcaaaagct gctatgaaaa gcctcagctt gggaagatag 660
atttttttcc ccccaattac aaaatctaag tattttggcc cttcaatttg gaggagggca 720
aaagttggaa gtaagaagtt ttatttttaag tactttcagt gctcaaaaaa atgcaatcac 780
tgtgttgtat ataatagttc ataggttgat cactcataat aattgactct aaggctttta 840
ttaagaaaac agcagaaaaga ttaaactctg aattaaagtct ggggggaaat ggccactgca 900
gatggagttt tagagtagta atgaaattct acctagaatg caaaattggg tatatgaatt 960
acatagcatg ttgttgggat tttttttaat gtgcagaaga tcaaagctac ttggaaggag1020
tgctataaat ttgccagtag ccacagatta agattatatc ttatatatca gcagattagc1080
tttagcttag ggggaggggt ggaaagtttg gggggggggt tgtgaagatt tagggggacc1140
ttgatagaga actttataaa cttctttctc ttaataaaag acttgtctta caccgtgctg1200
ccattaaagg cagctgttct agagtttcag tcacctaatg acaccacaa aacaatatga1260
atatggagat cttcctttac ccctcaactt taatttgccc agttatacct cagtgttgta1320
gcagtactgt gatacctggc acagtgcctt gatcttacga tgccctctgt actgacctga1380
aggagacctt agagtccttt ccttttttga gtttgaatca tagccttgat gtggtctctt1440
gttttatgtc cttgttccta atgtaaaagt gcttaactgc ttcttggttg tattgggtag1500
cattgggata agatttttaac tgggtattct tgaattgctt ttacaataaa ccaattttat1560
aatctttaaa tttatcaact ttttacattt gtgttatatt cagtcagggc ttcttagatc1620
tacttatggt tgatggagca cattgatttg gagtttcaga tcttccaaag cactatttgt1680
tgtaataact tttctaaatg tagtgccttt aaaggaaaaa tgaacacagg gaagtgactt1740
tgctacaaat aatgttgctg tgttaagtat tcatattaaa tacatgcctt ctatatggaa1800
catggcagaa agactgaaaa ataacagtaa ttaattgtgt aattcagaat tcataccaat1860
cagtgttgaa actcaaacat tgcaaaagtg ggtggcaata ttcagtgcct aacacttttc1920
tagcgttggg acatctgaga aatgagtgc caggtggatt ttatcctgc aagcatgttg1980
ttataagaat tgtgggtgtg cctatcataa caattgtttt ctgtatcttg aaaaagtatt2040
ctccacattt taaatgtttt atattagaga attctttaat gcacacttgt caaatatata2100
tatatagtac caatgttacc tttttatttt ttgttttaga tgtaagagca tgctcatatg2160
ttaggtactt acataaattg ttacattatt tttcttatg taataccttt ttgtttgttt2220
atgtggttca aatatattct ttccttaaac tcttaaaaaa aa 2262

```

000250" 6954950

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1301 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

accagcaagc aaccggccga agtctggaag ggcgccggag ccccgcgaa cggcccgacg 60
gagcgagga ggttccccgc cgccgcgcgc ttggccccga gtctctgcag ccgcagccgg 120
cacggaggga gccagccccg accttgcccc gctgcggccc gcggctcccc gccaaacccc 180
cctcaggaaa gaggttttaa aatcaaagat gggaaaatcg gagaaaattg cccttcccc 240
tggccagctt gttcatggta tacacttgta tgagcaacca aagataaaca gacagaaaag 300
caaatataac ttgccactaa ccaagatcac ctctgcaaaa agaaatgaaa acaacttttg 360
gcaggattct gtttcatctg acagaattca gaagcaggaa aaaaagcctt ttaaaaatac 420
cgagaacatt aaaaattcgc atttgaagaa atcagcattt ctaactgaag tgagccaaaa 480
ggaaaattat gctggggcaa agtttagtga tccaccttct cctagtgttc ttccaaagcc 540
tcctagtcac tggatgggaa gcactgttga aaattccaac caaaacaggg agctgatggc 600
agtacactta aaaacgctcc tcaaagttca aacttagatt tcagatttca gtatgtgtgt 660
aaaacataat ttttcccata tccctggact cttgagaaaa ttggtacaga aatggaaatt 720
tgccctgttg caacatacaa ttgcaaaaaga tgagtttaaa aaattacata caaacagctt 780
gtattatatt ttatatattg taaatactgt ataccatgta ttatgtgtat attgttcata 840
cttgagaggt atattatagt ttgttatga aagtatgtat ttgcccctgc ccacattgca 900
ggtgttttgt atatatataa tggataaatt ttaagtgtgt gctaaggcac atggaagacc 960
gattttatgt gcacaaggta ctgagatttt tttcaagaaa cagctgtcaa atctcaaggt 1020
gaagatctaa atgtgaacag tttactaatg cactactgaa gtttaaatct gtggcacaat 1080
caatgtaagc atggggtttg tttctctaaa ttgatttgta atctgaaatt actgaacaac 1140
tcctattccc atttttgcta aactcaattt ctggttttgg tatatatcca ttccagctta 1200
atgcctctaa ttttaatgcc aacaaaattg gttgtaatca aatttttaaa taataataat 1260
ttggccccc ctttttaaaa aaaaaaaaa aaaaaaaaa a
1301

```

000260 " 69594960

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 274 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

attgcgagtt	ttttgtttg	ttgtttcaat	gtgacttgtc	gtttatttca	atgaaaattt	60
aaatgattct	tacaaatcct	ctgaaaagta	aaactgatac	ttttataaac	agaagtatat	120
gcaaacagtc	acaatatgca	ttaggcagac	tgacgatatt	tcttacatgc	cagggagttc	180
tccatcccca	gcaaacacat	cttatctgaa	agtgtttttt	ctcctataaa	ttggcatcta	240
agggattttt	aaaaagtcaa	aaacagtggc	aggg			274

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2073 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ctattacaca tgagggttttt aatgtattta gacctgacaa taggggtgtc acttagatgt 60
gatctcagtg ttgtgggtaa ctttgtgtgt ctttaattcg aaatctggaa catagatgat 120
gattttttcc tttgaattaa cttaatgtgt tctcttcctt acagatttca gaacttatat 180
ttccacctct tccaatgtgg caccctttgc ccagaaaaaa gccaggaatg tatcgaggga 240
atggccatca gaatcactat cctcctcctg ttccatttgg ttatccaaat cagggaagaa 300
aaaataaacc atatcgccca attccagtga catgggtacc tcctcctgga atgcattgtg 360
accggaatca ctggattaat cctcacatgt tagcacctca ctaacttcgt ttttgattgt 420
gttggtgtca tgttgagaaa aaggtagaat aaaccttact acacattaaa agttaaaagt 480
tcttactaat agtagtgaag ttagatgggc caaacatca aacttatttt tatagaagtt 540
attgagaata atctttctta aaaaatatat gcactttaga tattgatata gtttgagaaa 600
ttttattaaa gttagtcaag tgcctaagtt tttaatattg gacttgagta tttatatatt 660
gtgcatcaac tctgttgat acgagaacac tgtagaagtg gacgatttgt tctagcacct 720
ttgagaattt actttatgga gcgtatgtaa gttatttata tacaaggaaa tctattttat 780
gtcgttgttt aagagaattg tgtgaaatca tgtagttgca aataaaaaat agtttgaggc 840
atgaaaaaaaa 850

```

(2) INFORMATION ON SEQ ID NO. 60:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2091 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

000260" 6954559 " 092000

aagagacaga ctattaactc cacagttaat taaggacgta tgttccatgt ttatttggtta 60
aagcagtgtg aatagccttc aagcatgtga ataattcttc atcttccccg ccgctttttg 120
tttctttcag gtagacacct tttaaaatgc agaactaact gaggcatttc agtaactttg 180
ctttcaaata aataaagtca aatgtatgga aacattttgt gccctactct ccataccccg 240
tgtactcaaa ttctctactg tatgaattat gctttaagta gaattcagtg ccaaggagaa 300
cttggtgaaa taaattattt taattttttt tttatctttt acaaagccat ggatttttatt 360
tggttgatgt gtgctctgta cacaagccat ttcaatagga tggagctgtt aattattttc 420
caaagagtaa tagacatgca aaagtttcaa taaaaactgg gccattaaca aataaattaa 480
taaactaata agcattccct tctaggtttt tgccaaactg cctatccaat aacaaatttg 540
agaatcgttg aaaaagctag ttatattttc gagaaatgat tttcattatt gaaactgttc 600
tccttagcag gccattttcc ctttttcttg ggagtttagc aagtttagga gagaatagtc 660
atgaaaagaa aggggaagaa ggggagaagg gaagagggtta aaaaataagt gctcagacct 720

atgaacgtaa tccctttgct agaaatatct aagagcagct cagcttggtt gaaactgagt 780
tttgtcatct tccatatttg caggaaggta ttttctgact tgcaatgcag ctagatgtaa 840
aattttattt tatcatccta gaaagccttg actagaaaaa tgaataaata ttgagggttt 900
cctgtccata tctggcttgc atgtgccaga aagcagagaa tagaaaatgt aatctccaac 960
atccaagcat cgaaacccaa ggggtaggca attctatgta ggttttgac atgaagtttg 1020
gtgcatcttg gtttatgctg gctcaactgc tattaacact ctctggctta tagtctcttc 1080
attctattag acaagcacgt atcgaacact tgcttcgcac aaggctcttt agttaacaat 1140
ttagcagcta ctgtttgtgt taaacacact tttcaccaa taggttctga ggcaaacgag 1200
agcaatgact atttaaagaa aggcctttcc agcatcactt acacatccca aaactaaaaa 1260
gatcaactct tccaactgag aaaagactcc tggctttgaa tggaaactta cagcagagag 1320
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cgttttaata atacatctta ttatttttct agtagagaaa ctacaaatca gcctcttcaa 1440
catttatata cagtttaata agcctcttgc aagttacttg ttctctcacc tgagggtattt 1500
ttttctctcc cacttgccc ctgttctctc ctctctcttc tccctttgca agaggaaata 1560
tttaacatat ttgggtccaa cttcaataat gtaataatta atacattaaa agcatttaac 1620
ttcttttcta gaaaaatgca caggctaagg catagacaaa acaaagagaa atgctgagaa 1680
atgtgccaact ggagacaagc aatctgaata aatatttgcc aaaagttctt tttatgtcat 1740
atagtgtcag gatttgaagg agctattttt ttttaatgtt gcaactagca actcatcttc 1800
ggaagacaca gccaggagaa tgaagtagaa gtgaaagggt tataaatcca tttgtaagca 1860
tttatcccat atattttaaa ttcaagaaaa attgtgttta tctttagaat tttgtattca 1920
atactttatg tactatgtga ctcatgcttc tggataaata aagcaccaaa tatgtatctg 1980
taaccacaat cacacatatt atattaaata tatatctata taacagccaa aaaaaaaaaa 2040
agaagagaag aaaaagaaag gagagggggg gggagagaag gggggggagg t 2091

(2) INFORMATION ON SEQ ID NO. 61:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2952 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000250"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

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ctcgtcccaa accaggacac cctctctaca gtaaatacat gcgtggggat gtacttgtga 60
tgctgaagca gacggaaaat aattacttgg agtgccaaaaa gggagaagac actggcagag 120
ttcacctgtc tcaaatgaag attatcactc cacttgatga acatcctaga agcagacca 180

acgatccaag ccacgctcag aagcctgttg acagtgggtgc tctcatgct gtcgttcttc 240
atgatttccc agcagagcaa gttgatgatt tgaacctcac ttctggagaa attggtttat 300
cttctggaga agatagatac agattggtac agagggaact gtagaaacca gattggcata 360
tttctgcca actatgtcaa agtgattatt gatatcccag aaggaggaaa tgggaaaaga 420
gaatgtgttt catctcattg tgttaaaggc tcaagatgtg ttgctcgggt tgaatatatt 480
ggagagcaga aggatgagtt gagtttctca gagggagaaa ttattattct taaagagtat 540
gtgaatgagg aatgggcccag aggagaagtt cgaggcagaa ctgggatttt cccctgaac 600
tttgtggagc ctgttgagga ttatcccacc tctggtgcaa atgttttaag cacaaggta 660
ccactgaaaa ccaaaaaaga agattctggc tcaaactctc aggttaacag tcttccggca 720
gaatggtgtg aagctcttca cagttttaca gcagagacca gtgatgactt atcattcaag 780
aggggagacc ggatccagat tctggaacgt ctggattctg actggtgcag gggcagactg 840
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cagcatgggg aggtctcacac acagaagtgt cacgtggaca tctgttttaa tcagcacaag 1440
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acattttagc ttttattgtt tttttttcc cattgtccaa aaagttaagc aacaagtggc 2460
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atttcatgag aaatcaatga tttaaagcat tatccaaatt aaattatcat ttgcagcaaa 2700
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ttttaacatc ttatattgaa gattctgaaa acctatcttt attagaggaa aatctcaatc 2820
ttcagttttg gccttctgtc accagaatga taagtgaat agttgtaaat ctacttgaca 2880
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gaatggaggt gg
2952

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(2) INFORMATION ON SEQ ID NO. 62:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2313 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09646569.092000

(2) INFORMATION ON SEQ ID NO. 63:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1650 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

ccgcggggct gggggagctc ggggagcctg cgggaccggg ggagcccga ggcaggggg 60
atcccgcggc ggcgccaggg aggcggagga gcaggcggtg gaggcgaggc aggaagagga 120
gcaggacttg gatggtgaga aggggccatc atcggaaggg cctgaggagg ggggacggag 180
aaggctttct cttcaaatac agccccggga agctgagggg aaaccagtac aagaagatga 240
tgaccaaaga ggagctggag gaggagcaga gaactgaaga ataacgaagt tatccttagc 300
gtcctcctaa aggtttttcc ttttggcatc ttaaaagctt gagagataaa acggaaaccc 360
cagagaggag tctgggcagg ctcccagggt gcatgctgcc tccataaatc tgctgagctc 420
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gccctgtgta gagatgttca tgtctgttcc tgtgggtcac tttgttaagc tgaagagttt 540
taagaggtag agctcagacc ctggactggg atttttctta ccaactcaac ttgctatcca 600
cacacctgc acaccttaga taaaaagaac attttaaaag cagagtccac tttcactcca 660
gtctccctc ttttgcctc actgaagcca aaccacagaa gactttgagg aatgagagac 720
aaatgaggta gagctcacct gtgtcacca gctccgtcag ggtggtcagc cgacctttt 780
ccctgggaac cccacttctc tctgtggctg gcttggttgt cgggggtgag atgccatatt 840
gattacaggg cagcaaagaa ccagtaccag gaatttactt gaccattccc cttatttttc 900
atctagagga atctcggatt cagccctttc attgctaaga caccttttca ctgaggttct 960
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tcagatcagt ctcaaattggg tttcttgga ttttatattt gacaatattt atactatacc 1140
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acagcaatag tcatgccctt gtccaggctg ggatctaatt gatacaatag gtcgttgact 1440
ccctcctagt agagctatct aggtttgtct ggaaagtttc cgacctggc ttataggcac 1500

cacacctcat gtactcctca tggcttggat ctctgtattc agcctttgtt cagtccaata 1560
aactttgagt agatgatctc aaaaaaaaaa aaaaaaaaaa gggagaaggg aagaaggaga 1620
gggcacaaag gcggaatggg ggtgagcttt

```

1650

00645569 " 092000

(2) INFORMATION ON SEQ ID NO. 64:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2851 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

cgccccgcgc cgccccgcgc ctgtcagctc cctcagcgtc cggccgaggc gcggtgtatg 60
ctgagccgct gccgcagccg gctgctccac gtcctgggcc ttagcttccct gctgcagacc 120
cgccggccga ttctctctctg ctctccacgt ctcatgaagc cgctgggtcgt gttcgtccctc 180
ggcggccccg gcgcgggcaa ggggacccag tgcgcccgcg tcgtcgagaa atatggctac 240
acacaccttt ctgcaggaga gctgcttcgt gatgaaagga agaaccaga ttcacagtat 300
ggtgaactta ttgaaaagta cattaaagaa ggaaagattg taccagttga gataaccatc 360
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cgatgtcttg agaggggaaa gagtagtggt aggagtgatg acaacagaga gagcttgga 600
aagagaattc agacctacct tcagtcaaca aagccaatta ttgacttata tgaagaaatg 660
gggaaagtca agaaaataga tgcttctaaa tctgttgatg aagtttttga tgaagttgtg 720
cagatttttg acaaggaagg ctaattctaa acctgaaagc atccttgaaa tcatgcttga 780
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cttaagtga tttgtggacc aaatttcaaa ggaacttttt gtgtagtcag ttcttgcaac 1200
atgtgttttg taaacaaact caaaatggat tcttaggagc attttagtgt ttattaaata 1260
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aaagttgtat gacagggcat attctttgct tccaagattt ggggtggggg cactaggggt 1380
tcagagcctg gcagaattgt cagcttttagt ctgacataat ctaagggtat ggggcaaggaa 1440

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000250" 6554960

tcacatctaa tgcttgtgtt ccttatactc tattatatag tgttattcat gattcagctg1500
 atcttaacaa aattcgtagc agtggaacct tgaaatgcat gtggctagat ttatgctaaa1560
 atgattctca gttagcattt tagtaacact tcaaagggtt ttttttgttt gttttctaga1620
 ctttaataaaa gcttaggatt aattagaaga agcaatctag. ttaaatttcc catttgtatt1680
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 ggaatttgtt ttcgccttac ttttttttct tctgtcacia tgctaagtgg tatccgaggt1980
 tcttaatatg agatttataaa tcttaaaaatg tttcttattt tcagcactta catcatttgg2040
 tacacagggc caaatagggc aaataatttt gtctttgtat aatagatttg atattttaaag2100
 tcaactggaaa taggacaagt taatggatgt ttttatattt taatagaatc atttatttct2160
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 aggcttttgc ttttgtttgc ttttaagtag aaaaacatgt tggcaacatt gagttttgga2640
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 ccaagaatgt tttgagtttt ttgaaagacc ccaatttaag ccttgcttat ttttaatta2760
 tttccattca gtgatgttg atgtatatca attatttagt aaataatctc aataaatttt2820
 gtgctgtggc ctttgctaaa aaaaaaaaaa t 2851

(2) INFORMATION ON SEQ ID NO. 65:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09646569.092000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

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attccaaaca tggcggctcc actagggggt atgttttctg ggcagccacc cgggtccccct 60
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agaccttcca gcagtacttt ggtggacgag ttggagtcac ctttcgaggc ttgctttgca 180

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gatcagtgtg tccagaagtt tctggatatt gcaagacaga cagaatgttt tttcttacaa 300
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ctaaggaatg aattacagcg gaaagatgca ctagtccaga agcacttgac aaagctgagg 420
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ttagttttat gctcccattg aaaaattttc cactattttt ataagctgtt aatttcttga 720
gtactttata acatgtctgt agcttgata aaccaagtaa gtattttttt tttgtcttta 780
gogaagttta gactgtgaat atgatgacac agattctttt ttatggtggc tttgcttgtt 840
ttaaattttt gcatgacttt tcatcttttt atgtgtgttt cctgtagttt gatccgaagg 900
aaaagagtat agtagcctga gaatcaggag atgggagttt tagtcgtagg ccttatgata 960
attacccccg ggtggtgtgt agaaaagtat gtaaatttgc tctgttttaa gactttgaac 1020
tacctcaaga agaggaatct aatacaatat ttgtaatgtt tccagaaaaa a 1071

```

(2) INFORMATION ON SEQ ID NO. 66:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2375 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09546569 "092000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

agcttgccaa ttctgtaact ccttgggata tcttgctgag ctttaattgca gctgcccactc 60
atgatctgga tcatccaggt gttaatcaac ctttccttat taaaactaac cattacttg 120
caactttata caagaatacc tcagtactgg aaaatcacca ctggagatct gcagtgggct 180
tattgagaga atcaggctta ttctcacatc tgccattaga aagcaggcaa caaatggaga 240
cacagatagg tgctctgata ctagccacag acatcagtcg ccagaatgag tatctgtctt 300
tgtttaggtc ccatttggat agaggtgatt tatgcctaga agacaccaga cacagacatt 360
tggttttaca gatggctttg aaatgtgctg atatttgtaa cccatgtcgg acgtgggaat 420
taagcaagca gtggagtga aaagtaacgg aggaattctt ccatcaagga gatatagaaa 480
aaaaatatca tttgggtgtg agtccacttt gcgatcgtca cactgaatct attgccaaaca 540
tccagattgg ttttatgact tacctagtgg agcctttatt tacagaatgg gccaggtttt 600
ccaatacaag gctatccag acaatgcttg gacacgtggg gctgaataaa gccagctgga 660

agggactgca gagagaacag tcgagcagtg aggacactga tgctgcattt gagttgaact 720
cacagttatt acctcaggaa aatcggttat cataaccccc agaaccagtg ggacaaaactg 780
cctcctggag gtttttagaa atgtgaaatg gggctcttgag gtgagagaac ttaactcttg 840
actgccaaag tttccaagt agtgatgcca gccagcatta tttatttcca agatttcctc 900
tgttggatca tttgaaccca cttgttaatt gcaagacccg aacatacagc aatatgaatt 960
tggttttcat gtgaaacctt gaatatgcaa agcccagcag gagagaatcc gaaaggagta1020
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tcttgtaact tccactaagt tctctctgag aaaatggaaa tgtgaagtgc ccagcctctg1200
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tgtagcatga ttgtgaagga accactcaaa caaatttaaa gatcaaactt tagactgcag1320
ctctttcccc ctggtttgcc tttttcttct ttggatgcca ccaaagcctc ccatttgc1380
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tccagtgcg tttggcaatg caattttttt tagcaattag tttttaattt ggggtgggag1500
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tttactact gtacacttga cctgcacatg cgagaaaaag gtggaatgtt taaaacacal620
taatcagctc aggttatttg ccaatctgaa ataaaagtgg gatgggagag tgtgtccttc1680
agatcaaggg tactaaagtc ctttcgctg cagtgaagtga gaggtatgtt gtgtgtgaat1740
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gtaatttggt ttaaattgtt ttatgtatag taagcacaac tgtaatctag ttttaagaga2160
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00646569 "092000

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cagctgctat	gccgtgga	tctgtttac	tttctgcac	tgctcctgca	agactctgga	120
gccagtcctg	aggtcctaca	tctccgaag	caagctcttc	tagaagttga	tagctttcca	180
atgattagac	gaattgattc	tttctgtgac	tcatcagttc	atttcctgta	aaattcatgt	240
cttgctgttg	atttgtgaat	aagaaccaga	gcttgtagaa	accactttaa	tcatatccag	300
gagtttgcaa	gaaacaggtg	cttaacacta	attcacctcc	tgaacaagaa	aaatgggctg	360
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caagtcaaaa	tcttctatgt	tccaagtcag	aactttgaga	gaactgttat	ggggctatag	900
ggatccattt	ttgagtttgg	ttccgtaccc	tgttactacc	acagttgggtc	tgttttatcc	960
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atcatatggt	gtgctagaca	tcagcaaatg	caaagaaggg	agacctgtgt	acatttcact	1380
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tgcaaaaacgg	ctgcagggtc	acctattggt	caagccatca	gaaaaaattc	agtgagttct	1560
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gtaaatctat	gtaagtaagt	gggaataaca	tctggtatca	acttatcttt	agcttaatgt	1680
caccaatcag	tattaaatgc	ttatgactaa	tttcacagat	tttggaatgg	ttttatgggt	1740
ttatttgagc	atttgatagc	atctctgatt	ttgttagctg	cgcaaatatt	tctatgacaa	1800
taattaattt	ttggaattca	tat				1823

(2) INFORMATION ON SEQ ID NO. 68:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2403 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260" 69594966

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

actaagattt tatgttggag atacttcttt aaataaccta cagcttgggt ctatggcttg 60
tgacccccag attcatggag gggcttttagc aatcagcttt gtacatcatc atttttctga 120
atgaccaatc ccactaaaca tctttgaagt cggcctagag aggtccttca gatgattcag 180
aaatagctgg cttgtctgag tccagatttc tcatcaactg gcaatacaaa ggaaaatatg 240
gtacaggagt tagttagaaa ggtcttattg attttacttc tacttttcac tacagttaca 300
ggtagaatac tgtaggaagt cagtgcgaag tgcattgctt attgatagat attgattggt 360
tttcagtctc tggggtcagt tttgtggttt ctgctttctt gcctaaatca aagactatgt 420
caagtcaaca acactgaaaa ctgcttttgc cctccactct tacagctgtg cctaataata 480
attaattaat aaacgcacag ccctatgtga acagacagga atttcttggt caatgtggag 540
caaagtgaat ggtctccttc cgcaagtctt ttttaacttc atatctggag tacaagggtg 600
gacctctggc ttaccacata cactatgcta aagtcattcag ccactgctac tacatcttgc 660
cagaagggtt ccctcgccaa caaacagttg aaatttaagg gaagaagcaa aagctaaact 720
gtctttgacc ctaagataga tagaaagcta tttatttggt ttcagtgttc aaggcatgac 780
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atgagggtaa ataaatatgt gttataacaa gtaaacctgt gttgcaagaa tataccatga 960
agattaaagt aggctgggtt tcatttccat ctcccccac atctcattga atttgatggt 1020
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taaaatgcct tatatattaa agagtaagtg caataatatg aaatagcctg tacattttaall 1140
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ttaaaaaaaaa taaacactct gcttactact tgaaaaaaaa aaaaaa 1246

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(2) INFORMATION ON SEQ ID NO. 71:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1950 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```

ggggtcgcgg gccctgattg cgccgtttcc ccgcgcagag ctgcgcggcg ccccgacggg 60
ccccggagca gcggcccccg gccggcccg cctcagcctg gagctccagc taccacatg 120
caccttacct gggttccgcc cggtcctga gtccccacaa aatggctgat ggaggaagcc 180
ccttcctagg tcggagggac tttgtctacc ctctctcaac ccgagaccct agtgctcta 240
acggaggggg cagcccagcc aggagggaag agaagaagag aaaggccgcc aggtcaagt 300
ttgacttcca ggcgagtc ccgaaggagc tgactctgca gaagggtgac attgtctaca 360
tccacaagga ggtggacaag aactggctgg agggagagca ccacggccgc ctgggcatct 420
tccctgctaa ttatgtggag gtgctgcccg cagatgagat ccctaagccc atcaagcccc 480
cgacctacca ggtgctggag tatggagagg ctgtggccca gtacaccttc aagggggacc 540
tggaggtgga gctgtccttc cgcaaggagg agcacatctg cctgatccgc aaggtgaacg 600
agaactggta cgaggagcgc atcacgggca cggggcgcca aggcattatc cctgccagct 660
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cagaccccaa gtccccacc cccatcctgc tccagcgttt cctctaacag ggaccagctc 1500
tccgctttgc cccacgggg ttctctaac cagaaccagc ttcttagcct cgtagagacc 1560
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tgccaagtcc tggccctggc cctggcatat caccgcgac tgtggggcca ggcaccacta 1800
gcctggctca aatattcccc agggagactg ctgtgtgctg cccgcctgcc tgctggctct 1860
ccccagccc cacatccct ctggaagaga atgtaaaata aacctggaca caagggaaag 1920
aaaaaataag attggggggg aggaaaaaaa

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00250"5954560

(2) INFORMATION ON SEQ ID NO. 72:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 814 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

cgggggagag cggggcctgc gcggtagtg gacccgaccc tgtctccagt gggcgtcttg 60
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gtcctaactc tgcggggctg cagcttcctg catgatgctg gggagcttg cgcctgaccc 180
aggatctaga aggcactctg ggcaggccgc gtcgcgccc cgaagggtacc caaccctctg 240
ggatagatgc aggaagcgat ggtaagacc cattttcacc caacttctcg ccgcagtctg 300
gcttaccaca cgctcctccc cattcccagt gagccgcttt ttgcagcacc aggcgaacac 360
ttacaccagt gctttgtaaa ggaatcttat tgtccacccc gtgtcttggc aaaagaacag 420
tgatcacaca gattcctact tgggctcttt cctttaatct tcggaggctg agtttgccca 480
actcaggttt aaccaccaag gactctgaga gctggcagg ctgagtaacc ctggtaacaa 540
ttctcttcac cttatcaaaa cctgagctaa aaccaatgca tcagctgatg atgacagcag 600
agagtggcag ggctgaggac ccaaagtcac ttcccaggct ggcggagaat aaactgccag 660
ggagaagaat gagaagacag gagacaaact gtttggaag ctaaatcttc cctcttaatg 720
aataaagggt tttgccttgt cttaaaaaat aacaggaaga agcagggaaa aataaataac 780
ttatggtaat ctggaattgt attttgtaat atta 814

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(2) INFORMATION ON SEQ ID NO. 74:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

09646569 "092000

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

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tgggacagcc eggcccgtag cccggcccgcc tgctgcgccc gcccgaggcc ccgcccgtgg 60
agagcgccga gccgctgggg cccgcgcccg atctgtgggc cgacgtggac ctcaccgagt 120
tcgaccagta cctcaactgc agccggactc ggcccgacgc ccccgggctc ccgtaccacg 180
tggcactggc caaactgggc ccgcgcgcca tgctctgccc agaggagagc agcctgatct 240
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gggcttttcc aggaagcccc agcccaggac ctggttgagc agttgccagg gttacatttt 600
tgaagcacct gctccttttc ttgcagtgtt tttctacaa ccagattgta ttaatatatt 660
ttactttgcc cttttaaaaa atatacctaa tacaatatat ttaattttta attaaactct 720
taaacttttc ttccaagaga aaggagc                                     747

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(2) INFORMATION ON SEQ ID NO. 76:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2419 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

09646569 "092000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

cttttgccac ccagtaccgg atagtggacc tgctgggtgga agccgcgggg cccggccagg 60
 gatcgtcgca tggaatttct ggtggagcct gtccccaagg aagggttccg ggtacctcag 120
 gccgagtggg gcagggcagt tctgctttat tcagccctg catgagcgga tgctaaggcc 180
 ggggtgtctc ctggcctcgg gctgaggcct cttcccggct gtctgcccct ggctgcgct 240
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ccccggggctg agtgcgtgtg ctttctggtg gggggcgatg gaaacaggaa accaagcagt 360
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 tccccacggg acctggttcc caggtgaaaa tgaaaggagg ggagaagttg agaacagaac 480
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 aggcgcggag acatttctga gcatgaggac gagctacagc agctcctggg gtggggctgc 660
 ctgcgggatg gcgggagagg atgccctgga gaaccgtcct ccagtggtg aaggcccttt 720
 tccctgagga gtgggcattc tgggccagcc ggcgtgtgct tcgtgcctcc acgtgggcca 780
 gccccagctg ctccgtgttt cctggcggtg gcaatttact gtgctgctga gtgtgaggtc 840
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 gaggcagggt cttaccaca ggcgccttcc tctgtccttc ctgctcttcc ttctctgccc 1260
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 gaaggagaag tgagtttgcc aaggatatgg ggcaggaggc tccctctgct gacccctgc 1860
 agcctggagc cagcccgggg actgtcctgg gtggagggca ggtgaacaca agctgctgcc 1920
 ggggactgtc ctgggtggac ggcagggtgaa cacaagcggc tgccgcatgt agccactcac 1980
 tcgacttttt ttcagctgtg accattcctg ggagctcttt gagcctttct gtctcatttg 2040
 gaaccagggg gaaccaggaa ggggtcctg gcctctctgt gtccctctgca gtgggggttg 2100
 tggggggcgc agatccacgc cttgctgccc ttctttcatg aagtctgttt tttaagtgtc 2160
 ggttcccccg aatattttat gcagaggagg gaaaatttat agtggcaatt attttctcac 2220
 agtctggtga gcaggcaatt aattaggagt aagggggcct agtagagcgt ggcgtgtggc 2280
 agaatcgac cgccccggct cccagccca ccgcatgca gggctcgcgt gcgggaaaac 2340
 taatatgccg gcgtttaagc ctgtgcccct ctgctgggtg taactgcgct gaaataaatg 2400
 atctgacaat gtgaaaaaa 2419

(2) INFORMATION ON SEQ ID NO. 77:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 366 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

IASARLEEVTV GK LQVARNLI MRGTEMCPKS EDVWLEAARL QPGDTAKAVV AQAVRHL PQS 60
 VRIYIRAAEL ETDIRAKKRV LRKALEHVPN SVRLWKA AVE LEEPEDARIM LSRAVECCPT 120
 SVELWLALAR LETYENARKV LNKAREN IPT DRHIWITAAK LEEANGNTQM VEKIIDRAIT 180
 SLRANGVEIN REQWIQDAEE CDRAGSVATC QAVMRAVIGI GIEEEDRKHT WMEDADSCVA 240
 HNALECARAI YAYALQV FPS KKS VWLRAAY FEKNHGTRES LEALLQRAVA HCPKAEVLWL 300
 MGA KSKWLAG DVPAARSILA LAFQANPNSE EIWLAAVKLE SENDEYERAR RLLAKARTVP 360
 PPPGCS 366

(2) INFORMATION ON SEQ ID NO. 78:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 62 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

MRTSKFILFI FSDVG NGLGF KRELEEGMFD SHRRFLQOMP LLAISHFFPQ ILPTEAQFT 60
 VS 62

(2) INFORMATION ON SEQ ID NO. 79:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 39 amino acids
 (B) TYPE: Protein

00646569 "092000

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

RPRLYKAKRK TTNGVVLCCI ALHKIRNRCL TIEFVFCEF

39

(2) INFORMATION ON SEQ ID NO. 80:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 25 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

KTPSLQSKTK NNKWSCAMLY CFAQN

25

(2) INFORMATION ON SEQ ID NO. 81:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 29 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

DPVSTKQNEK QQMELCYVVL LCTKLGTGV

29

000260"69594960

(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

PKRRVSDTSS GPTPCMEPIL GRTHYSQLRK KS

32

(2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

LGQDSHQHIT HVLLGREKQY IPVERSQSIG GRNVVKGGRG YAAAPSVPEV AVIP

54

000260"69594966

(2) INFORMATION ON SEQ ID NO. 84:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 54 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GDQAHREQGK EQAMFDKKVQ LQRMVDQRSV ISDEKKVALL YLDNEEEEND GHWF

54

(2) INFORMATION ON SEQ ID NO. 85:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 116 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GTRHPLSLSH KPAKKIDVAR VTFDLYKLNQ QDFIGCLNVK ATFYDTYSLS YDLHCCGAKR 60
IMKEAFRWAL FSMQATGHVL LGTSCYLQQL LDATEEGQPP KKGASSLIPT CLKILQ 116

(2) INFORMATION ON SEQ ID NO. 87:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 71 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

000260"69594960

(vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

NRGGVGFGVG WSLPFELLIF MSRLQNSRVG LTMWGGGGSS LFFYFQVHSW GWWGGRRIP L 60
PKPLVCAELA L 71

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

YRHEPLYPAF PYKIQRENFY TFIPQIKQVL SSYRALARSI CKRNLKFSCR IKLDK 55

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

LATHSPQKSH QCAHCEKTFN RKDHLKNHLQ THDPNKMAFG CEECGKKYNT MLGYKRHLAL 60
 HAASSGDLTC GVCALELGST EVLLDHLKAH AEEKPPSGTK EKKHQCDHCE RCFYTRKDVRI120
 RHLVVHTGCK DFLLCQFCAQR FGRKDHLTRH TKKTHSQELM KESLQTGDLL STFHTISPSF180
 QLKAAALPPF PLGASAQNGI ASSLPPEVHS LTLSPPEQAA QPMQPLPESL ASLHPSVSPG240
 SPPPPPLPNHK YNTTSTSYSP LASLPLKADT KGFCNISLFE DLPLQEPQSP QKLNPGFDLA300
 KGNAGKVNLP KELPADAVNL TIPASLDLSP LLGFWQLPPP ATQNTFGNST LALGPGESLP360
 HRLSCLGQQQ QEPPLAMGTV SLGQLPLPPI PHVFSAGTGS AILPHFHAF R 411

(2) INFORMATION ON SEQ ID NO. 90:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 314 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

KRCQRKQPLR GIGILKQAID KMQMNTNQLT SIHADLCQLC LLAKCFKPAL PYLDVDMMDI 60
 CKENGAYDAK HFLCYYYYGG MIYTGLKNFE RALYFYEQAI TTPAMAVSHI MLESYKKYIL120
 VSLILLGKVQ QLPKYTSQIV GRFIKPLSNA YHELAQVYST NNPSELRLNV NKHSETFTRD180
 NNMGLVKQCL SSLYKKNIQR LTKTFLTLSL QDMASRVQLS GPQEAKEYVL HMIEDGEIFA240
 SINQKDGMSV FHDNPEKYNN PAMLNIDQE MLKCIELDER LKAMDQEITV NPQFVQKSMG300
 SQEDDSGNKP SSYS 314

(2) INFORMATION ON SEQ ID NO. 91:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 58 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

VLQEKIKIKK EKKEKIKFKN CFENVQIKSN ILIIHLHVLL NILIMWMFTL CMILA EYH 58

(2) INFORMATION ON SEQ ID NO. 92:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 201 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

MDLSLLWVLL PLVTMAWGQY GDYGYPPYQQY HDYSDDGWVN LNRQGFYSYQC PQGQVIVAVR 60
 SIFSKKEGSD RQWNYACMPT PQSLGEPTEC WEEINRAGM EWYQTCSNNG LVAGFQSRFY120
 ESVDREWFQF YCCRYSKRCP YSCWLTTEYP GHYGEEMDMI SYNDDYYIRG ATTTFSAYER180
 DRQWKFIMCR MTEYDCEFAN V 201

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 247 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

MGNGLSEERG NNFNHISPIP PVPHPRSVIQ QAEEKLHTPQ KRLMTPWEES NVMQDKDAPS 60
 PKPRLSPRET IFGKSEHQNS SPTCQEDEED VRYNIVHSLP PDINDTEPVT MIFMGYQQAE120
 DSEEDKKFLT GYDGIIHAEL VVIDDEEEED EGAEKPSYH PIAPHSQVYQ PAKPTPLPRK180
 RSEASPHEHT NHKSPHKNSI SLKEQEEESLG SPVHHS PFDA QTTGDGTEDP SLTALRMRMA240
 KLGKKVI 247

000260"69594960

(2) INFORMATION ON SEQ ID NO. 95:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 188 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

MPVLREYLMS GGICPVSRTD IDYLLSKNGS GNAIIIVVGG AAESLSSMPG KNAVTLRNRK 60
 GFVKLALRHG ADLVPIYSFG ENEVYKQVIF EEGSWGRWVQ KKFQKYIGFA PCIFHGRGLF120
 SSDTWGLVPY SKPITTVVGE PITIPKLEHP TQDDIDLYHT MYMEALVKLF DKHKTKFGLP180
 ETEVLEVN 188

(2) INFORMATION ON SEQ ID NO. 96:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 290 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

RGAGTQPGPL LKKPYQPRIK ISKTSVDGDP HFVVDFFLSR LTVCFNIDGQ PGDILRLVSD 60
 HRDSGVTVNG ELIGAPAPPN GHKKQRTYLR TITILINKPE RSYLEITPSR VILDGGDRLV120
 LPCNQSVVVG SWGLEVSUSA NANVTVTIQG SIAFVILHL YKKPAPFQRH HLGFIYANSE180
 GLSSNCHGLL GQFLNQDARL TEDPAGPSQN LTHPLLLQVG EGPEAVLTVK GHQVPVWVKQ240
 RKIYNGEEQI DCWFARNNA KLDIGEYKDY LASHPFDTGM TLGQGMSREL 290

000260"69594960

(2) INFORMATION ON SEQ ID NO. 97:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

NQFTSCILFC DGGHWRELLF QSIMSSHWTL KILLVPLFYI SLEFPSGFVL CLANDLGYHF 60
SSRVRS 66

(2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

VP GALPLAVG PPPPPSGFPR NVQPRRPSQS LGRVMSAGPD KRPLGTLCCF VSFL 54

(2) INFORMATION ON SEQ ID NO. 99:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

000260"69554960

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

FFLYFNQVFY WSGNCKIYKF LKGISCLKAS IALYPRS LIQ TNTQNT EKS

59

(2) INFORMATION ON SEQ ID NO. 100:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 98 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

MGNKEPGSHG HRSDADPSRF SPVLPPAVQL GVVREEGRGG SCFFSWGRGP VSSTWLFPKG 60
SKREGLGEKT MERGPAKENR EEVSGLISLL SRCSGSLI 98

(2) INFORMATION ON SEQ ID NO. 101:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 117 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

MGKGLGEDGQ QRARESWTSQ RRRPQQVQSR AATSCPAGCL EGRGQRRVMS LQLGEGPSEL 60
HVAFSQREQE GRIGRENNGE GTCEGKQGGG ERFDQPAITV FWLSYLARRL RDRYITS 117

0000260" 6954960

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 152 amino acids
(B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

SEARNAPSGT AQTFAMGFMT GTISSMYQTK AVIIAMIITA VVSISVTIFC FQTKVDFTSC 60
TGLFCVLGIV LLVTGIVTSI VLYFQYVYWL HMLYAALGAI CFTLFLAYDT QLVLGNRKHT120
ISPEDYITGA LQIYTDIIYI FTFVLQLMGD RN 152

(2) INFORMATION ON SEQ ID NO. 105:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 66 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

HLLSPPHILG TAFSSTGNGT DGQKTSITFM KGLLELPGKK ACLGELGRCR QCGWAGGQPV 60
VLLPAQ 66

(2) INFORMATION ON SEQ ID NO. 106:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 91 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

000260" 6954960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

PTSLIWPTTM FCSVHVLFKS IILNWLPSFKL NQTLKAWSSH TGPTFPHGNY ERAPAQQGLS 60
 RSLPPPLPVP QIWPLLRKIR TATGPSEPKP T 91

(2) INFORMATION ON SEQ ID NO. 107:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 41 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

LLPSFFLHFS LSIYFPHPTF LEQPLVLQEM ALMDRRLALP S

41

(2) INFORMATION ON SEQ ID NO. 108:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 471 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

000260" 6954960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

NELKASGGEI KIHKMEQKEN VPPGPEVCIT HQEGEKISAN ENSLAVRSTP AEDDSRDSQV 60
 KSEVQQPVHP KPLSPDSRAS SLSESSPPKA MKKFQAPARE TCVECQKTVY PMERLLANQQ120
 VFHISCFRCS YCNNKLSLGT YASLHGRIYC KPHFNQLFKS KGNVDEGFGH RPHKDLWASK180
 NENEEILERP AQLANARETP HSPGVEDAPI AKGGVLAASM EAKASSQQEK EDKPAETKKL240
 RIAWPPPTTEL GSSGSALEEG IKMSKPKWPP EDEISKPEVP EDVDLDLKKL RRSSSLKERS300
 RPFTVAASFQ STSVKSPKTV SPPIRKGWSM SEQSEESVGG RVAERKQVEN AKASKKNGNV360
 GKTTWQNKES KGETGKRSKE GHSLEMENEN LVENGADSDE DDNSFLKQQS PQEPKSLNWS420
 SFVDNTFAEE FTTQNOQSQD VELWEGEVVK ELSVEEQIKR NRYYDEDEDE E 471

(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 94 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

RKMLRAALPA LPIPRCKYTL FLIAHMGPPY LLALVLMKLS WPWERCLPGR HSCLVQAKPL 60
 CNASPFWCYE VPLCRRFHQQ LVTVPSTRTC FEIS 94

(2) INFORMATION ON SEQ ID NO. 113:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 324 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

000260" 6954960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

GLSTFQNWLP STPATSWGGL TSSRTTDNGG EQTALSPQEA PFSGISTPPD VLSVGPEPAW 60
 EAAATTGKLA TDVATFTQGA APGREDTGLL TTTHGPEEAP RLAMLQNELE GLGDIFHPMN120
 AEEQAQLAAS QPGPKVLSAE QGSYFVRLGD LGPSFRQRAF EHAVSHLQHG QFQARDTLAQ180
 LQDCFRLEIK AQQAPEGQPR LDQSGASAE DAAVQEERDA GVLSRVCGLL RQLHTAYSGL240
 VSSLQGLPAE LQQPVGRARH SLCELYGIVA SAGSVEELPA ERLVQSREGV HQAWQGLEQL300
 LEGLQHNPPPL SWLVGPFALP AGGQ 324

(2) INFORMATION ON SEQ ID NO. 114:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 148 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

IAMTPPNATE ASKPQGTTCV PPCDNELKSE AIIEHLCASE FALRMKIKEV KKENGDKKIV 60
 PKKKKPLKLG PIKKKDLKKL VLYLKNGADC PCHQLDNLSH HFLIMGRKVK SQYLLTAIHK120
 WDKKNKEFKN FMKKMKNHEC PTFQSVFK 148

(2) INFORMATION ON SEQ ID NO. 115:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 45 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

PVIYSVLIRS EIRYKISRPV TTDFIKSESL ILACLYLISE RMSTL

45

(2) INFORMATION ON SEQ ID NO. 116:

00260"6954960

- PDCESFMYFN LDSVFLRVLS MKLADSRQDS FFHHGWLISP

(2) INFORMATION ON SEQ ID NO. 117:

- TNEHTLTSYL QLPFSFNRIV KASCILI

(2) INFORMATION ON SEQ ID NO. 119:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 135 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

(2) INFORMATION ON SEQ ID NO. 122:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```
EACAH TLSCP  ALARLGRARR  RPWMSHRTSS  TFRAERSFHS  SSSSSSAATS  SSASRALPAQ  60
DPPMEKALSM  FSDDFGSFMR  PHSEPLAFPA  RPGGAGNIKT  LGDAYEFAVD  VRDFSPEDII120
VTTSNNHIEV  RAEKLAADGT  VMNTFAHKCQ  LPEDVDPTSV  TSALREDGSL  TIRARRHPHT180
EHVQQTFRTE  IKI
```

(2) INFORMATION ON SEQ ID NO. 124:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 38 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

MATFYPLFPN GGGTYPEVVN DFPLKLLYFT NLNYFVLM

38

(2) INFORMATION ON SEQ ID NO. 125:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 65 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

MWLFHDAGIR SAGGLSLLSC GSWPLPSGYH RLQDTNGQQK NVTLLILSSS SIGTKLPSRP 60
REILC 65

(2) INFORMATION ON SEQ ID NO. 126:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 250 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

ETRVKTSLEL LRTQLEPTGT VGNTIMTSQP VPNETIIVLP SNVINFSQAE KPEPTNQGGD 60
SLKKHLHAEI KVIQTQILC GMMVLSLGII LASASFSPNF TQVTSTLLNS AYPFIGPFFF120
IISGSLSIAT EKRLTKLLVH SSLVGSILSA LSALVGFIIL SVKQATLNPA SLQCELDKNN180
IPTRSYVSYF YHDSLYTTDC YTAKASLAGT LSLMLICTLL EFCLAVLTAV LRWKQAYSDF240
PGVSVLAGFT 250

(2) INFORMATION ON SEQ ID NO. 128:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 61 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

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(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

MHTCQIYYIS TNVTFLEFFVL DVRACSYVRY LHKLLHYFFL CNTFLFVYVV QIYSFLKLLK 60
K 61

(2) INFORMATION ON SEQ ID NO. 129:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 211 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

PASNRPKSGR APEPREPARR SAGGSPPPPP WPRVPAAAAG TEGASPD LAP LRPAAPGQTP 60
LRKEVLKSKM GKSEKIALPH GQLVHGIHLY EQPKINRQKS KYNLPLTKIT SAKRNENNFW120
QDSVSSDRIQ KQEKKPFKNT ENIKNSHLKK SAFLTEVSQK ENYAGAKFSD PPSPSVLPKP180
PSHWMGSTVE NSNQNRELMA VHLKTLLKVQ T 211

(2) INFORMATION ON SEQ ID NO. 131:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 48 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

MILTNP LKSK TDTFINRSIC KQSQYALGRL TIFLTCQGV L PSQQTPLI

(2) INFORMATION ON SEQ ID NO. 132:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 78 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

LGIFLHQYVI FNQNVKFLN SLPAIVIVPS WPTWFPDVVN NINASAVGPL LRCLRRNFVL 60
AISINFV FYL QFGRRKVT 78

(2) INFORMATION ON SEQ ID NO. 133:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 72 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

MDMAKTKFLR RHLSKGPTAD ALMLFTTSGN QVGHDGTITM AGNEFNKNFT FWLKITYWCK 60
KIPNQIKSYC FD 72

(2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 87 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

LN VFSS LQIS ELIFPPLPMW HPLPRKKPGM YRGNGHQNH Y PPPVPFGYPN QGRKNKPYRP 60
IPVTWVPPPG MHC DRNHWIN PHMLAPH 87

(2) INFORMATION ON SEQ ID NO. 137:

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

MYGNILCPTL HTPCTQILYC MNYALSRIQC QGELGEINYF NFFFILYKAM DFIWLMCALY 60
TSHFNRMELL IIFQRVIDMQ KFQ 83

(2) INFORMATION ON SEQ ID NO. 138:

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

RPKPGHPLYS KYMRGDVLVM LKQTENNYLE CQKGEDTGRV HLSQMKIITP LDEHLRSRPN 60
 DPSHAQKPVD SGAPHAVVLH DFPAEQVDDL NLTSGEIVYL LEKIDTDWYR GNCRNQIGIF120
 PANYVKVIID IPEGNGKRE CVSSHCVKGS RCVARFEYIG EQKDELSFSE GEIILKEYV180
 NEEWARGEVR GRTGIFPLNF VEPVEDYPTS GANVLSTKVP LKTKKEDSGS NSQVNSLP AE240
 WCEALHSFTA ETSDDL SFKR GDRIQILERL DSDWCRGRLQ DREGIFPAVF VRPCPAEAKS300
 MLAIVPKGRK AKALYDFRGE NEDELSFKAG DIITELESVD DDWMSGELMG KSGIFPKNYI360
 QFLQIS 366

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 68 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

MNPYISIIIVF IVFLCSENYP WNNMLRITGS SPYLHFLSVL GVLVNSYVLI LFNSEFLTQH 60
 FRERIQAG 68

(2) INFORMATION ON SEQ ID NO. 140:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 28 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

FFFFFFLLLK FFFNKDKGFN NFCATILN

28

(2) INFORMATION ON SEQ ID NO. 141:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 22 amino acids
 (B) TYPE: Protein

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(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

EGTTRKKDKY ILSLENASRQ KY

22

(2) INFORMATION ON SEQ ID NO. 142:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 46 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

MPFLRKFDRL VRTSDHQISL KWVSWNFIFD NIYTIPNSFA VLRFVG

46

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(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

MEGWGMSSIN PYGMHSQWPS HLGLEPLVQG LGENRPHGNS HTVIAFNTEP RVPKQQ 56

(2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

MNISTQGRAK GVPRILLAKG QVLIEGLELS RFMEAACLTG ACPDSSLGFP FYLSSF 56

(2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

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- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

MPKGKAFRRT LRITSLFFSS LLLQLLFGH HLLVLVSPQL PGAVFEGEAF SVPPPQALPM 60
 MAPSHHPSA PLPASPPPPA PPPPWRRRGI PLAFGLPRSR RLPQLPQPR 109

(2) INFORMATION ON SEQ ID NO. 146:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 247 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

RPAPAPRCQL PQRPAEARCM LSRCSRLLH VLGLSFLLQT RRPILLCSPR LMKPLVVFVL 60
 GGPGAGKGTQ CARIVEKYG Y THLSAGELLR DERKNPDSQY GELIEKYIKE GKIVPVEITI120
 SLLKREMDQT MAANAQKNKF LIDGFPRNQD NLQGWNKTMD GKADVSFVLF FDCNNEICIE180
 RCLER GKSSG RSDDNRESLE KRIQTYLQST KPIIDL YEEM GKVKKIDASK SVDEVFDEVV240
 QIFDKEG 247

(2) INFORMATION ON SEQ ID NO. 147:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 181 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

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```
IPNMAAPLGG MFSGQPPGPP QAPPGLPGQA SLLQAAPGAP RPSSSTLVDE LESSFEACFA 60
SLVSQDYVNG TDQEEIRTGV DQC IQKFLDI ARQTECFFLQ KRLQLSVQKP EQVIKEDVSE120
LRNELQRKDA LVQKHLTKLR HWQQVLEDIN VQHKKPADIP QGSLAYLEQA SANIPAPLKP180
T
```

(2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 236 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```
MLRDLQLQL  RNVTHHVSVT  KQLPTSEAVV  SAVSEAGASG  ITEAQARAIV  NSALKLYSQD  60
KTGMVDFALE  SGGGSILSTR  CSETYETKTA  LMSLFGIPLW  YFSQSPRVVI  QPDIYPGNCW 120
AFKGSQGYLV  VRLSMMIHPA  AFTLEHIPKT  LSPTGNISSA  PKDFAVYGLE  NEYQEEGQLL 180
GQFTYDQDGE  SLQMFQALKR  PDDTAFQIVE  LRIFSNWGHP  EYTCLYRFRV  HGEPVK      236
```

(2) INFORMATION ON SEQ ID NO. 149:

- ```
(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 57 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:
```

MEWSPSASLF NPHIWSTRVD LWLTTYTMLK SSATATTSCQ KVS LANKQLK FKGRSKS 57

(2) INFORMATION ON SEQ ID NO. 150:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 52 amino acids  
(B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

MHLALTSYSI LPVTVVKSRS KINKTFLTNS CTIFSFLPV DEKSGLRQAS YF

52

(2) INFORMATION ON SEQ ID NO. 151:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 377 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

LRRFPAQSSP APRRAPEQRP PAGPASAWSS SYPHAPYLGS ARSLSPHKMA DGGSPFLGRR 60  
DFVYPSSTRD PSASNGGGSP ARREEKKRKA ARLKFDFQAO SPKELTLQKG DIVYIHKEVD120  
KNWLEGEHHG RLGIFPANYV EVLPADEIPK PIKPPTYQVL EYGEAVAQYT FKGDLEVELS180  
FRKGEHICLI RKVNNENWYEG RITGTGRQGI FPASYVQVSR EPRLRLCDDG POLPTSPRLT240  
AAARSARDPS APSALRSPAD PTDLGGQTSP RRTGFSFPTQ EPRPQTQNLG TPGPALSHSR300  
GPSHPLDLGT SSPNTSQIHW TPYRAMYQYR PQNEDELELR EGDRVDVMQQ CDDGWFVGVS360  
RRTQKFGTFP GNYVAPV

377

(2) INFORMATION ON SEQ ID NO. 152:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 39 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

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(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

WDPTLSPVGV LGPGSILGCG PGKGSPGAK

39

(2) INFORMATION ON SEQ ID NO. 153:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 58 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

MQEAMVKTHF HPTSRRSLAY HTLLPIPSEP LFAAPGEHLH QCFVKESYCP PRVLAKEQ 58

(2) INFORMATION ON SEQ ID NO. 154:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 41 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

GGEPGLRGSG TRPCLQWASW APALFWAAGL GRARRVPNEL S

41

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## (2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 75 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

MMLGSLAPDP GSRRHSGQAA LRPRRYPTLW DRCRKRWLRP IFTQLLAHV LTRSSFPV 60  
SRFLQHQAANT YTSAL 75

## (2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 50 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

GASRACAVVG PDPVSSGRLG PRLYSGLRAW EGLAGCQMSC PNSAGLQLPA

50

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## (2) INFORMATION ON SEQ ID NO. 157:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GTPGPYPGPL SPPPEAPPLE SAEPLGPAAD LWADVLTET DQYLNCSTR PDAPGLPYHV 60  
 ALAKLGPRAM SCPESSLIS ALSDASSAVY YSACISG 97

## (2) INFORMATION ON SEQ ID NO. 158:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 173 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GLFPAVCPWP ALDLLSGPQW QRGPGPGAGV GDPGLSAVAF WWGAMETGNQ AVGSQRWSLR 60  
 GEWRAFCFCL VPPHGTWFPG ENERRGEVEN RTFHKGYFLI GCKMLMPRMM IFFPADETIR120  
 KGLRLWQVGF GAGAETFLSM RTSYSSSWG AACGMAGEDA LENRPPSVEG PFP 173

## (2) INFORMATION ON SEQ ID NO. 159:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein

00645559-092000

(iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

GCGGGTGACG CGACGACGGC TCGACACTTT GCTACGGAGT GCATCGGACG TCGAAGCCTA 60  
 GAGTCTCTGC GTCTTTCCCT CTTCCGCTGC CTCATTCTT TCCTTCCTAG CCTTGGTCGT 120  
 CGCCGCCACC ATGAACAAGA AGAAGAAACC GTTCCTAGGG ATGCCCCGCGC CCCTCGGCTA 180  
 CGTGCCGGGG CTGGGCCGGG GCGCCACTGG CTTCACCACG CGGTCAGACA TTGGGCCCCG 240  
 CCGTGATGCA AATGACCCTG TGGATGATCG CCATGCACCC CCAGGCAAGA GAACCGTTGG 300  
 GGACCAGATG AAGAAAAATC AGGCTGCTGA CGATGACGAC GAGGATCTAA ATGACACCAA 360  
 TTACGATGAG TTTAATGGCT ATGCTGGGAG CCTCTTCTCA AGTGGACCCT ACGAGAAAGA 420  
 TGATGAGGAA GCAGATGCTA TCTATGCAGC CCTGGATAAA AGGATGGATG AAAGAAGAAA 480  
 AGAAAGACGG GAGCAAAGGG AGAAAGAAGA AATAGAGAAA TATCGTATGG AACGCCCCAA 540  
 AATCCAACAG CAGTTCTCAG ACCTCAAGAG GAAGTTGGCA GAAGTCACAG AAGAAGAGTG 600  
 GCTGAGCATC CCCGAGGTTG GCGATGCCAG AAATAAACGT CAGCGGAACC CACGCTATGA 660  
 GAAGCTGACC CCTGTTCTTG ACAGTTTCTT TGCCAAACAT TTACAGACCG GAGAGAACCA 720  
 TACCTCAGTG GATCCCCGAC AAACCTCAAT TGGAGGTCTT AACACACCCT ATCCAGGTGG 780  
 ACTAAACACT CCATACCCAG GTGGAATGAC GCCAGGACTG ATGACACCTG GCACAGTGAG 840  
 CTGGACATGA GGAAGATTGG CCAAGCGAGG AACACTCTGA TGGACATGAG GCTGAGCCAG 900  
 GTGTCTGACT CCGTGAGTGG ACAGACCGTC GTTGACCCCA AAGGCTACCT GACGGATTTA 960  
 AATTCCATGA TCCCGACACA CGGAGGAGAC ATCAATGATA TCAAGAAGGC GCGACTGCTC 1020  
 CTCAAGTCTG TTCGGGAGAC GAACCCTCAT CACCCGCCAG CCTGGATTGC ATCAGCCCGC 1080  
 CTGGAAGAAG TCACTGGGAA GCTACAAGTA GCTCGGAACC TTATCATGAA GGGGACGGAG 1140  
 ATGTGCCCCA AGAGTGAAGA TGTCTGGCTG GAAGCAGCCA GGTTCAGCC TGGGGACACA 1200  
 GCCAAGGCCG TGGTAGCCCA AGCTGTCCGT CATCTCCAC AGTCTGTCAG GATTTACATC 1260  
 AGAGCCGCAG AGCTGGAAC GGACATTCTG GCAAAGAAGC GGGTTCTTCG GAAAGCCCTC 1320  
 GAGCATGTTT CAAACTCGGT TCGCTTGTGG AAAGCAGCCG TTGAGCTGGA AGAACCTGAA 1380  
 GATGCTAGAA TCATGCTGAG CCGAGCTGTG GAGTGCTGCC CCACCAGCGT GGAGCTCTGG 1440  
 CTTGCTCTGG CAAGGCTGGA GACCTATGAA AATGCCCGCA AGGTCTTGAA CAAGCGCGGG 1500  
 GAGAACATTC CTACAGACCG ACATATCTGG ATCACGGCTG CTAAGCTGGA GGAAGCCAAT 1560  
 GGGAACACGC AGATGGTGGG GAAGATCATC GACCGAGCCA TCACCTCGCT GCGGGCCAAC 1620  
 GGTGTGGAGA TCAACCGTGA GCAGTGGATC CAGGATGCCG AGGAATGTGA CAGGGCTGGG 1680  
 AGTGTGGCCA CCTGCCAGGC CGTCATGCGT GCCGTGATTG GGATTGGGAT TGAGGAGGAA 1740  
 GATCGGAAGC ATACCTGGAT GGAGGATGCT GACAGTTGTG TAGCCACAA TGCCCTGGAG 1800  
 TGTGCAAGAG CCATCTACGC CCACTGCCCTG CAGGTGTTCC CCAGCAAGAA GAGTGTGTGG 1860  
 CTGCGCGCCG CGTACTTCGA GAAGAACCAT GGCACCTCGG AGTCCCTGGA AGCACTCCTG 1920  
 CAGAGGGCTG TGGCCCACTG CCCCAAAGCA GAGGTGCTGT GGCTCATGGG CGCCAAGTCC 1980  
 AAGTGGCTGG CAGGGGATGT GCCTGCAGCA AGGAGCATCC TGGCCCTGGC CTTCCAGGCC 2040  
 AACCCCAACA GTGAGGAGAT CTGGCTGGCA GCCGTGAAGC TGGAGTCCGA GAATGATGAG 2100  
 TACGAGCGGG CCCGGAGGCT GCTGGCCAAG GCGCGGACAG TGCCCCCACC GCCCGGGTGT 2160  
 TCATGAAGTC TGTGAAGCTG GAGTGGGTGC AAGACAACAT CAGGGCAGCC CAAGATCTGT 2220  
 GCGAGGAGGC CCTGCGGCAC TATGAGGACT TCCCCAAGCT GTGGATGATG AAGGGGCAGA 2280  
 TCGAGGAGCA GAAGGAGATG ATGGAGAAGG CGCGGGAAGC CTATAACCAG GGGTTGAAGA 2340  
 AGTGTCCCCA CTCCACACCC CTGTGGCTTT TGCTCTCTCG GCTGGAGGAG AAGATTGGGC 2400  
 AGCTTACTCG AGCACGGGCC ATTTTGGAAG AGTCTCGTCT GAAGAACCCA AAGAACCCTG 2460  
 GGCTGTGGTT GGAGTCCGTG CGGCTGGAGT ACCGTGCGGG GCTGAAGAAC ATCGCAAATA 2520  
 CACTCATGGC CAAGGCGCTG CAGGAGTGCC CCAACTCCGG TATCCTGTGG TCTGAGGCCA 2580  
 TCTTCCTCGA GGCAAGGCCC CAGAGGAGGA CCAAGAGCGT GGATGCCCTG AAGAAGTGTG 2640  
 AGCATGACCC CCATGTGCTC CTGGCCGTGG CCAAGCTGTT TTGGAGTCAG CGGAAGATCA 2700  
 CCAAGGCCAG GGAGTGTTTC CACCGCACTG TGAAGATTGA CTCGGACCTG GGGGATGCCT 2760  
 GGGCCTTCTT CTACAAGTTT GAGCTGCAGC ATGGCACTGA GGAGCAGCAG GAGGAGGTGA 2820  
 GGAAGCGCTG TGAGAGTGCA GAGCCTCGGC ATGGGGAGCT GTGGTGCGCC GTGTCCAAGG 2880  
 ACATCGCCAA CTGGCAGAAG AAGATCGGGG ACATCCTTAG GCTGGTGGCC GGCCGCATCA 2940  
 AGAACACCTT CTGATTGAGC GGTTCCTATG GCCGCTCTCC GTGGGGCAGG GTTGGGCCGC 3000  
 ATGTGGAAGG GCTCTGAGCT GTGTCTCTCT TCATTAAAG TTTTATGTG TCGTGTGAGA 3060  
 AAAAAAAGA AAAGAAAAA GGGGGCGCCC GGGGGC 3096

## (2) INFORMATION ON SEQ ID NO. 162:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1987 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```

CTTTGAATTT TAGAATGTCA TGTGTTCTTT TAAAAAATT AGCTCCCCAT CCTCCCTCCT 60
CACGCGCTCC CTCCCTCCTT CTCTCTCTCT CTCTCTCTCC CTCTCTCACA GACACACACA 120
CACACACACA CACACGCACA CGCACGTCCA CACTCACATT AAATAAAAGC TTTATTTGAA 180
GCAAAGCTAG CCAAAATTCT ACGTTACTTT TCCCTTGACT GGATCCCAAG TAGCTTGGAA 240
GTTTTTGTGC CCAGGAGAGT AAATAACTGT GAACAAGAGG CTCTGCCCTT AGGTCTTTGT 300
GGCTGTTTAA GTCACCAACA ATAGAGTCAG GGTAAGAAGT AAAAACACTT TCATAGCCTC 360
ATTCATTCAC TTAGAAGTGG TAATAATTTT TCCCTAATGA TACCACTTTT CTTTTCCCCC 420
TGTACCTATG GGACTTCCAG AAAGAAGTTA AATTGAGTAA AATCATCAGA AACTGAATCC 480
ATGTAAGAAA AAATAATTGT TGAAGAAAGA AGTTGATAGA ATTCAAAAAG GCCATCTTTT 540
TGCTTTCACA TCAATAAAAT TTACCAAGTA ATAGATCAGT ACTCACTAAT ATTTTGTAGA 600
CCATAGTTGT CTGGTCAGAA AAATTATATT AAATTAGTAA ATTCTAGAAG CTCTTTAAAA 660
GGGAAGTTTT CTTTCTTCTC CAATTATAGG AGTTGATTTT TACTTTGCAA AGTGGCTCGG 720
TCCTCATGAG CATCTGCATG TTGACTCTTC AGTTAAGAAA ATTGTTGTTC ATTTAGGGAG 780
GTGGATATTC TGATGAAGAT CTTTATCCTA AACCTTCCTA CTATCCTTGT CTTATTCATC 840
AAGCAGATAT TTTAGTCAAG AATTCAGAG AAGGCTGCTC CTAAAATGTC TACTTGACGC 900
CCAATACAGT AGCTAAACT ATCCATTCTG GGGTCTGGCT TTAGAAATCA TCTTTGTGGG 960
AAGACCTAAT TCTTCACAGC AAGGATCTCA GGCATGCCTT CTAGATTTGT TCCCTCTGAG1020
GGGCAGGAAT GAACTGTAGA AATGTTTTAA GGACCCAGAA ACCCCATATG TCTCATTCCA1080
TGAATATAGG TGAGAGAATT CTTTCCTAAG AGGGTTTGAT ACCAATAGGG GAAAATGTAA1140
AATGTTTCACT CTTTATGACA ACCTGGCATA AAGGAGTCAA TTCTTATGAA AGAGACACAA1200
GGGCCTTATG GCCAGGGTTT CTTGGGACAA GACTCTCACC AGCACATCAC ACACGTTCTC1260
CTTGGAAGAG AGAAGCAGTA CATCCCGGTT GAGAGGTCAC AAAGCATTAG TGGGAAGAAAT1320
GTGGTAAAGG GGGGAAGGTG TTATGCGGCT GTCCTCCG TCCCAGAGGT GGCAGTGATT1380
CCATAATGTG GAGACTAGTA ACTAGATCCT AAGGCAAAGA GGTGTTTCTC CTTCTGGATG1440
ATTATCCCA AAGCCTTCCC ACCCAGGTGT TCTCTGAAAG CTTAGCCTTA AGAGAACACG1500
CAGAGAGTTT CCCTAGATAT ACTCTGCCT CCAGGTGCTG GGACACACCT TTGCAAAATG1560
CTGTGGGAAG CAGGAGCTGG GGAGCTGTGT TAAGTCAAAG TAGAAACCCT CCAGTGTGTTG1620

```

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GTGTTGTGTA GAGAATAGGA CATAGGSTAA AGAGGCCAAG CTGCCTGTAG TTAGTAGAGA1680
AGAATGGATG TGGTTCTTCT TGTGTATTTA TTTGTATCAT AAACACTTGG AACAAACAAAG1740
ACCATAAGCA TCATTTAGCA GTTGTAGCCA TTTTCTAGTT AACTCATGTA AACAAAGTAAG1800
AGTAACATAA CAGTATTACC CTTTCACTGT TCTCACAGGA CATGTACCTA ATTATGGTAC1860
TTATTTATGT AGTCACTGTA TTTCTGGATT TTTAAATTAA TAAAAAAGTT AATTTTGGAA1920
AATCAAAAAA AAAAAAATAA AAAGTCGACC GGCAGCGAAT TTAGTAGTAG TAGTAGTAGT1980
AGTAGGC

```

## (2) INFORMATION ON SEQ ID NO. 163:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

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GGGCCGGGCA GCCCAGCTGA AGGCAATAAG CTGGGCTCAC CGCTGCAGCA GAGTTCTGTG 60
CTAGCCGGGC ATAGGGGCGA GAGAAGGCCC AGAGGCGACG TCAGAGAGAA GCAACTGCGC 120
CCCGGTGAAG AGAAGCTCGC CCATCACCGG CTGGGAGCCA GCTTTCAGTG AAGATGGCAG 180
GGCCAGAACT GTTGCTTGAC TCCAACATCT GCCTCTGGGT GGTCTACCC ATCGTTATCA 240
CTCTTCGTAG ACATGATCCG CCACTACGTG TCCATCCTGC TGGAGAGCGA CAAGAAGCTC 300
ACCCAGGAAC AAGTATCTGA CAGGGGACGA GGCACCCACA GTCCCTCTCC CATAAGCCTG 360
CCAAGAAGAT TGATGTGGCC CGTGTAACTT TTGATCTGTA CAAGCTGAAC CCACAGGACT 420
TCATTGGCTG CCTGAACGTG AAGGCGACTT TTTATGATAC ATACTCCCTT TCCTATGATC 480
TGCACTGCTG TGGGGCCAAG CGCATCATGA AGGAAGCTTT CCGCTGGGCC CTCTTCAGCA 540
TGCAAGCCAC AGGCCACGTA CTGCTTGGCA CCTCCTGTTA CCTGCAGCAG CTCTTCGATG 600
CTACGGAGGA AGGGCAGCCC CCAAGGGGCA AGGCCTCATC CCTATCCCG ACCTGTCTGA 660
AGATACTGCA GTGAAAGCCC AAGTCCTTGG AAGCTTTCCC CAGTGAAGGA CTGACTGGGG 720
GCCTCACGCT TAACTGGTAG TGCCCAACAAG CCTGGCAGCT GTAGAGCCGC GAACCTCCCC 780
ACACCTCCCT CACCGCGCAG GACCCTGAGT GAGGAGGAGG AGCTGGAAAC CTGGGGTGGG 840
TTGGCCAAAG GAGAACCCTA AGCTCCTGGC CTGATCCAGC TCCTTCCTGC CCAAGGCAGC 900
TTAGCCCATC CAGACTGGTC CTGAAGTCTG TCCCTCCATT GGCATGAAGT CTGCCCCTTA 960
GCAATCCGGC CTCGCAGGCT GTACTTTCAT GGTGCTCTCT ACCTTCTGGC CCCCATCCCG 1020
GAACATTCCT GAGTGAATTC GCAAGCGCAC TAGCATGTGA TATTAGGGAG TTTGAATAA 1080

```

ATTATTGAGG CTGATGTAAA AAAAAA

1107

## (2) INFORMATION ON SEQ ID NO. 164:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GTGAATATGT GTGTATATGT GTGTGTATGT GTGTGTGGGG TTTGGGGTAG AAGGGAGGGA 60  
 GGGGGCAGGA CAGTGTGGAA TCTCTAGGGT GTATGGGTAG GTAGGGGGCA CAGTTAGTTC 120  
 TAAGTGGGCT TTTATGCTAA AAGCCTCTGG GGATATCTGT TTTGAAAATA AAGATAGGTG 180  
 TCCCCTCCTT GCTGTCATCT AGCCAGACA CTCTGCTTGC TCTCTGGCTG TCTGCTCCCT 240  
 GGGGAAGGCTT TAGGAGGACC ACCCAGGACA GGATGACCAT GCTGCCATCT GCTCTGGAGC 300  
 TGGGTCTCAG TGCAGAGGGA CAGTGAAGT GGATGGTTGC AGTCTCTGGT GGGAGGTGAG 360  
 GATAGAAGTG ATAAAGAGCT AAGAGGAGCT TCTGGGAGCC TTGGAGGAGG TCAGTCTTGC 420  
 AGTGGTGAAG CCAGGACATA GGAGATGGAG CAGGGCTGTG AGAGGAGGAG ATTCTGAGGA 480  
 GGATGCAGGG GAAATCTTGT CTGTTAATGA AATAGGGGTG GGGTGGGGTT TGGGGTGGGG 540  
 TGGTCATTGC CGTTTGAGCT GCTGATTTTC ATGAGTCGCC TTCAAACTC TCGTGTAGGG 600  
 TTGACAATGT GGGGGGGTGG GGGATCCAGC TTATTCTTTT ATTTTCAAGT CCATTCTTGG 660  
 GGCTGGTGGG GAGGCAGGAG AATACCCCTC CCTAAGCCCT TAGTGTGTGC CGAGCTTGCT 720  
 TTGTGATGTT GGCAGGGGAG GGGAGACCTG GGTGGTGAAG GAGTTCCTT TATCAAACCC 780  
 TTCAATGGGC ACAAATTGA GTGCTTGATT TTAGGTTTTA TTTTATTATG AATGTCCAAA 840  
 TCTGTGTTTC CCCCTGCCCT CCCAGACTGT GTGGCCAGTT GAAAGTGTCT GGTGTGTGTT 900  
 CATCTCTCCC TCATTCTTGG AGCAGGGCCT GAGACCTGC CACATCTCCT ATGCTCTGCA 960  
 TCCACGCCTC TTTTGGACAT TAAAGGTTGA TTGATGCAAA AAAAAAATAC AACGGGGTGG 1020  
 CTTGGGGAAG CCTGGGGTTG GCCGGCTTAT GGGGTGCGG CG 1062

(2) INFORMATION ON SEQ ID NO. 165:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2770 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

09646569 "092000

## (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CTACTATGGA TAATTTCAAA GTAGAATCAC TCTATGCTTA GAGTTTTGGC ACCAATGCTG 60  
 TAGGGCAGCA GAATCTATTC TCAGTAAAAT AACTTATGGT TTATTAGATA TTCTGTATTG 120  
 GATTTTACCA GCTTGACTTT TACTGCTCAG ATGCTTTCTT TCCCCCCTT AGACGCTGTA 180  
 ATTCTCTTGG GAAGAGTAAC TATTCTTAAG GTTTTACAG ATACCCACCT TAGTTGTAAA 240  
 TTGGATAGTT TATATTTCTG GGACTTTTTA AATGAAAATG TGGAATGTTA AGTTACAAAA 300  
 GACTTTTCAT CAGAAAATTT CAAACAAAGT AAACATGGCG TTTTATAGTC CTCTAAAATC 360  
 TAGGTGCTCC CACCCACCAA AGGCATATCC TGCAAAGGGC TGTGAACTAT CTTGGTGAAC 420  
 TGTCTTGGGT CCCCTTTCCA TGTATGTTTT CTTGTCCTG AAAACAAACA ACGCTGAGTT 480  
 TATCAAGAAA ATTTAAATTG GGGGATCATA ATAATTCCAA CCAAGTGACA ACTCTGACAT 540  
 CAAGGTTATT AGGAGCTGTA CATCCAATTC AAGTTTTATT TGCTGCTATT CTGGGAGAAT 600  
 AAACCTTGAT ATGGAGAATA AACTAATAAA CTTGTATCGA GGAAATCCAT AAAGTTATAA 660  
 ATTAGCCTGA AAAATATTTT AGGTAATGGT GTGGATTGGC CTGCTTTGAC TCTCAGCCAC 720  
 CAACAGAAAT CTTTGTCAAC TTTGTTCCCT AGCTAAAAGT AATTTTGTTA TAAACACAAA 780  
 GTGACTTTAA ACAGGTAAAA AACCCATTCC TATTTTTGTA CATTACCAA AGTTTTTCAT 840  
 ATACCTACAG AGCTAACTAA TTACAACCTGA TTTAATCCAC TCAAGTTTAG ACCAGTTAAA 900  
 CCCATAGGAT CCTGTATGGT TATCAATGTG ATGCCTTGCT TTTTATAAAA TAGGTATAAT 960  
 TGGGTCATAC ACTTGACGAG AGGGTGACTG TTTCTAGGGG AAGAAAACCC TTTAGATTGC1020  
 AGGTAACCTT CACTTTTTTT TTTTTAAATA TACACTTTAC ATTTGTATAA ATTATGCAGG1080  
 GTACTCCTAA CCCTGTAGAA ATGTATGACC TCTCACAAG TTGAGATTTG ATCCAAAGAG1140  
 AAATGCAAGT ATAAAAGAAT TAGATACCTT ATTATCTTTT AAGGTTTTTT TTTTTTTTG1200  
 GTAGAGATGG GGGTCTCACT GTGTTGCCCA GGCTGGTCTC AAACCTCTGG CCACAAGTGA1260  
 TCTTCTGCC TCAGCCTCCC AAAATGCTGA GATTACAGGC ATGAGCCACT GTACCCAGCC1320  
 TTTCTTATA AAATTCAAAG AGAAAATTTT TACACCTTTA TCCCTCAAAT AAAACAAGTG1380  
 CTCAGTTCTT ACCGTGCCCT TGCAAGGTCT ATATGTAAAA GAAATCTGAA ATTTAGCTGT1440  
 AGAATAAAAC TTGATAAATA AAAAGAAAAA ACATACATTT CTCCAGTTGG TTTGCTCTTT1500  
 GCTTGTTGAA GTAATAAACC GTTTTAAAGA GAAAATACTT GCTGTAAACC CCCAGTGCCT1560  
 TCAACTCTTT TGGCAGAATA TTTTAAAGA AATCCAGCAA GCAAACCTTG AGGTGCTAAT1620  
 GAAAGTAAAG GAAGGTGGTA TTTCTAGTTT TGGCAGAAAT GAAAAGTGTC TCACAAGAGA1680  
 CATCACTACC CACGTGGGGT CTGGCTGCTT TCTACCAAAG ACATTTAGAG AAGAAGTGAA1740  
 TTGAGTCAGG GTGATGGTGA AACTACATA TTTTATAGAT GGTTAAGTTG AGAATTAATT1800

ATGTTTATCA TGGATGGCTA CTAATACCAA GCTCATGATT GTTGCAAGCT CAACGTCTTA1860  
 GGCAGTAAAA CTTGTCTGCA GCACTAAAGG GGGAGAAACC CTTATATTTT GCAAAGTCTG1920  
 CATTCGTTAA ATTTATTGTA ACCTAATACC AAAAAGTCCG GTTTTTTCATA TTATTTCCCC1980  
 ACCTCCTACT TTTTTGTTT TTTTTTGCTA CTTGTAAAT AACCCTTCT AGAAAATAAG2040  
 CATTAACTGG AATGTTTCAA ACAATTTTGC TTCATTTTAC TATCAGCCAC TAGTGAAGTCT2100  
 TTACAGAGAT GTACATTTAA GATAAAATTA GCTTGTGCTA AGTGTTTTAA AAACATTGTT2160  
 TACTGTTAAA GGGGAATTGC ACATTATATT TAAGTGGGAT TGCTCCCTCC CTCAGTTCTT2220  
 TAAAAACAA GAGTCAAGGC TCACACCAAC TTGTAGGCTG TGGGAGCTTT GCCATAGGTA2280  
 GATACAATGT AGAAGTATAC TTTTTTAAAG CATGAAGAAG ACAAGGAAGT TCATTATAAT2340  
 GTACCAGGTA GAGGACATTA TTATTCAAAG GATTATGCAC AGCTCAGTGA AGATTGAAGT2400  
 ACAATTTTTC TCGCAGCTTT GTTGCTATTA TTTTCTTCTG CATAAATGTA TGCTCATTTT2460  
 ATTATGTGCC TTGCTCCCTG ATTGTGCAAA GCTATATATA TATATATATA TATAGATAGA2520  
 TAGATAGATA GATATATGAG AGAGATATAT TCAGTACTAC TGAGGATGTT TTTCTGAGGA2580  
 TGTTTTTGTT CTGCTGGATT AAGTTATTTT CCAAGTTACT CTTGCCAGTT ATGTCAGTAA2640  
 ACTATTGTAA TGGCTTAGCA CACTAGTCGT ACAGTCAGTG TAAATGTTTT TCATTTACAT2700  
 GTTTTCATTA TATCAGCTTA TCAAATCCTT AATAAAAAAA ATTCATAGAT TTCATTTAAA2760  
 CAAAAA

2770

0064559 092000

## (2) INFORMATION ON SEQ ID NO. 166:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 4242 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

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GGCCATTGAC CCTAGAGGTG AAACCGAAGC TCTGATGGAC TCTCACAGCT GGAGATGAAA 60
ATACGAGTTA TACACGGAGA ATGCAACCAC TGAGAAAACG GAACCGAATA GTCAAGAGGA 120
CAAGAATGAT GGTGGAAAAT CAAGAAAAGG GAATATAGAA CTTGCCTCAT CAGAACCACA 180
GCATTTTACA ACAAAGTGTG CTGATGCAG CCCGACCGTG GCCTTTGTGG AATTTCCCTC 240
CAGCCCCCAG CTGAAGAATG ATGTGTCGGA AGAAAAAGAC CAGAAGAAAC CAGAAAATGA 300
AATGAGTGGA AAGGTGGAGT TGGTGCTGTC ACAAAGGTG GTAAAGCCAA AATCTCCAGA 360
ACCGAAGCA ACGCTGACAT TTCCATTCTT GGACAAAATG CCTGAAGCCA ACCAACTACA 420
TTTGCCAAAT CTCAATTCTC AAGTGGATTG TCCAAGCAGT GAGAAGTCAC CTGTTATGAC 480
ACCTTTTAAG TTCTGGGCAT GGGACCCAGA AGAGGAGCGC AGGCGACAGG AAAAATGGCA 540

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09646569 . 092000

ACAGGAACAG GAACGTTTGC TCCAGGAGAG ATACCAGAAG GAGCAGGACA AGCTGAAAGA 600  
 AGAGTGGGAA AAGGCCCAAA AGGAGGTGGA AGAGGAAGAA CGCAGATACT ATGAGGAGGA 660  
 GCGTAAGATA ATTGAAGACA CTGTGGTTCC ATTTACTGTT TCTTCAAGTT CCGCTGACCA 720  
 GCTGTCTACC TCTTCTCCA TGAAGGAGG CAGTGGGACA ATGAATAAGA TAGACCTGGG 780  
 AAAGTGTCAA GATGAAAAAC AAGACAGAAG ATGGAAGAAA TCATTCCAGG GAGATGACAG 840  
 TGACTTATTG CTGAAGACTA GGGAAAGTGA TCGACTGGAG GAGAAGGGCA GCCTAACTGA 900  
 AGGGGCTTG GCTCATTTCTG GGAACCCCTGT ATCAAAGGA GTCCATGAAG ACCATCAGCT 960  
 GGATACCGAG GCTGGGGCCC CACACTGTGG AACAAACCCA CAGCTTGCTC AGGATCCATC1020  
 CCAGAATCAG CAGACATCAA ATCCAACGCA CAGTTCAGAA GATGTGAAGC CAAAAACCCT1080  
 CCCGCTGGAT AAAAGCATTG ACCATCAGAT CGAGTCTCCC AGTGAAAGGC GGAAGTCTAT1140  
 AAGTGGAAAG AAGCTGTGCT CTTCTGTGG GCTTCTTTG GGTAAAGGAG CTGCAATGAT1200  
 CATCGAGACC CTCAATCTCT ATTTTCACAT CCAGTGTTC AGGTGTGGAA TTTGTAAAGG1260  
 CCAGCTTGGA GATGCAATGA GTGGGACGGA TGTTAGGATT CGAAATGGTC TCCTGAACTG1320  
 TAATGATTGC TACATGCGAT CCAGAAGTGC CGGCAGCCT ACAACATTGT GACACGGCTT1380  
 TCAAGCTTCC GGATCACTCA CCATTTCTTT ACTGAGAGTG TCCCCTGGCA ACTGCTTAAC1440  
 AAAATCCCAA GCTCAGGGGC TTCTCAGCAT TTACCTAATT TCTGAAAGGC TCTTCTGAAA1500  
 GGTGGTATCT GTTCTTTCTG AGCACAGTGT TTATGTTTTT CCTGTTTATT GTTTTGGGTT1560  
 TTTGTTTTTT TTTTGTGATT TGCACAGTAT ACACAAAAGA ATATGGGGTT GTAATGATCC1620  
 TGAATAGCTC AAAAAAGGTT TTAGCATGGT CAAACAGGCT TATGGTTTAA AATGTGTTAT1680  
 TCTCTCTTT GGAATTAGC TAAATGATGC AATAAACCTG TTTTGTTTTA GAATGTCTAG1740  
 GAATTAAACA CTTTATGTTT ACAGAATTGA GCTGCAGAAA GTGCAAGACA TGCCAATTTG1800  
 AGACACACGG TCTTCTAAGA CTGAAGGATA AATTTAATGC ATTTTCAGAAA CTAAACATCA1860  
 CAGCAAGCTC TATCTCTGAG CTATAATTTG TTTTAAATGC AAAGACACTA GTTTGATAAT1920  
 ATATACTGTG ATCCTGAAAC ATTTGTGTTA CTTACCTTTG GAGGTAGAAA TTATACCAAT1980  
 AAATTATTGC ACCGTTAGTA TTAGATTCTG TGTACCTTGG AAGTTATGTC ATTAATATAG2040  
 GCTGGTTCAT CAAATAAAGC AAAACCTTGC AATATCAGCT AGATTTACAC TCCGGGACGT2100  
 TGCCCAAAGG TAGGAAGAAA GCAGAGGGAA ATATTTTCAAT AAGAGTCAAT GTGCAAGACA AGGCTCTGT2220  
 TCAAAATCTG TGAGGAAGTT TAATCTTCCA AAGAGTCAAT AAGAGACTTA ACATGAGGTA2280  
 TGCTGCTTC TCTCGAGGCA CTAGATTAGG AGTCTTCAAT TCATTAGGTG TGAGCACTGC TCACCCTTGC2340  
 TATGGAAGAT GAGGCACCGA GATAAGTTCA TCATTAGGTG AGGTGTCCAA AGAAAAGCGT TAAGTCCATC2400  
 TGGCAAGTTC TCCTTAAGGG CCTGAAGCAC TATGATGTGG TCAGCCCCTG GTCTGTGATC AGCAAGAACC2460  
 TTAATAGAAT CTATGTGGTA TATGATGTGG TCAGCCCCTG ATGAATACCT ACTCTCCTCC ATTCTCCATC2520  
 TACAGCACAG ATTATGCCCT GCCCACTTCA ATGAATACCT TGCCCATGGA GAAGTTTGA GAGGAACTCT2580  
 ACTTTTTTTG CTATCAAGAA TCCCGGACCT TGCCCATGGA GAAGTTTGA GAGGAACTCT2580  
 TGTGGAGAGC TGGTTTTATT TCTGCCCTGT TCTGCCAGTT TCAGCTGGCC AAGAAAGGAG2640  
 TCAAGTTATT AAAAAAGCATC ACAATGTAGA TCTCCAGGCT GGTTTTTTGT TTTTGTGTGT2700  
 TAAGACTGGG GAAAGGGGGA CTATTTATTC TGCCTTAAAT CAATGGCAAA TAAGTCAAGA2760  
 TGACATTTTG TGAATGTAGA CTATGGATAC ACTCCTAATA GATTGATGTA GTCATAAAG2820  
 GGGGTCAAGT AGATGTTTTT CTGTTATGTA AGCAATAATT TTTCCGTGTC TTATTGAGTA2880  
 TGGCTAGCGA TTATTTATTA CATGCTAGAT GGGTCTTTG CATGTGGGTT CCATATAGGT2940  
 GCAGAAATTT CCTCAGCCAC TGGAGGGATT TCGACCATAT TTGTCATTTG GATGAGCTGT3000  
 TATTAGATTG AAATCTACAC ATCATTTTCAT TAAAAATTGT GCCTTAGAAA ACGCAAAGCT3060  
 GTTGCACATG GCGATAAATT ATGGATGCAG TACATTGAAG AGAGATGAAG TCACTTCCAA3120  
 GTTTCCAAGA CTTCTCATGG AGGTGTTTGC TGTTTTACAG GAAAAAATAA AAATAAAAAA3180  
 AGAAAAAATA GAGAAAAAAT TAAATTCAAA AATTTGTTTT TGATAATGTG GATGTTTACA3300  
 AATATTTTGA TTATCCACCT GCATGTTTTA TTAATATTTT ACATGTACAA TATGGTCATT3360  
 CTTTGCATGA TATTAGCAGA GTACCACTAG TAATGCACAA CCATCCGTTA TGTAAGGATT3420  
 CATAACCGAT TTTTATAGAA TACTTTTTTAC ATGTGCAACT TTTATACATA TTTCTTAGTG3480  
 ACATGAATAT TGCACATTCC CTTCTGGTTT CACAAACCCA AAAAATAAAG CCCATTCTC3540  
 AGGCTCATTG TACATGTATT GAAGCTAGAA TCGAGTCAAG CACTAGTCAC CAGCACAGAA TAATCTCAA3600  
 CAACTGCAAA ATGTGCTTTC CCATAATGAA CTATTTTATAT TTGATTTATA TTTCAATTGG3660  
 CATTTTCTAA ATTCTAATTG CCAACTGTTT GATCTTGTTT TTTCCAATGC AGCATAATGA3720  
 AGTCTGTTAC ATGGCAGCTT AGGCAGACTA AATAATCTTT GAGATCCAG GAAAAAATAA ATGCTCTGCT3780  
 GTATGATCTA TTTCTTTTCA TGTGTTTGT TAAAAACAG GTGAGGCAAG TGAGTGATTT3840  
 CCATTGAGCT ATAATGTAAA TCTGATTTT TTTCTCATAC TCCAAAAGCT AGTCCCTACT3900  
 ATTGTTCTCT AGGAAGTATA TCTGATTTT TTTTCACTAG CGAACTTCCA TGACATTTCC3960  
 CTTTAATAAAA AATAATGGGT AACTTTTTGT

(2) INFORMATION ON SEQ ID NO. 167:

- ```
(i) SEQUENCE CHARACTERISTIC:
    (A) LENGTH: 2640 base pairs
    (B) TYPE: Nucleic acid
    (C) STRAND: individual
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
                    ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi)  ORIGIN:
    (A) ORGANISM: HUMAN
    (C) ORGAN:

(vii) OTHER ORIGIN:
    (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:
```

CTAGCAAGCA	GGTAAACGAG	CTTTGTACAA	ACACACACAG	ACCAACACAT	CCGGGGATGG	60
CTGTGTGTTG	CTAGAGCAGA	GGCTGATTAA	ACACTCAGTG	TGTTGGCTCT	CTGTGCCACT	120
CCTGAAAAAT	AATGAATTGG	GTAAGGAACA	GTTAATAAGA	AAATGTCGCT	TGCTAACTGT	180
GCACATTACA	ACAAAGAGCT	GGCAGCTCCT	GAAGGAAAAG	GGCTTGTGCC	GCTGCCGTTT	240
AAACTTGTCA	GTCAACTCAT	GCCAGCAGCC	TCAGCGTCTG	CCTCCCCAGC	ACACCCCTAT	300
TACATGTGTC	TGTCTGGCCT	GATCTGTGCA	TCTGCTCGGA	GACGCTCCTG	ACAAGTCGGG	360
AATTTCTCTA	TTTCTCCACT	GGTGCAAAGA	GCGGATTTCT	CCCTGCTTCT	CTTCTGTCAC	420
CCCCGCTCCT	CTCCCCCAGG	AGGCTCCTTG	ATTTATGGTA	GCTTTGGACT	TGCTTCCCCG	480
TCTGACTGTC	CTTGACTTCT	AGAATCGAAG	AAGCTGAGCT	GGTGAAGGGA	AGACTCCAGG	540
CCATCACAGA	TAAAAGAAAA	ATACAGGAAG	AAATCTCACA	GAAGCGTCTG	AAAATAGAGG	600
AAGACAAACT	AAAGCACCAG	CATTTGAAGA	AAAAGGCCTT	GAGGGAGAAA	TGGCTTCTAG	660
ATGGAATCAG	CAGCGGAAAA	GAACAGGAAG	AGATGAAGAA	GCAAAATCAA	CAAGACCAGC	720
ACCAGATCCA	GGTTCTAGAA	CAAAGTATCC	TCAGGCTTGA	GAAAGAGATC	CAAGATCTTG	780
AAAAAGCTGA	ACTGCAAATC	TCAACGAAGG	AAGAGGCCAT	TTTAAAGAAA	CTAAAGTCAA	840
TTGAGCGGAC	ACAGGAAGAC	ATTATAAGAT	CTGTGAAAGT	GGAAAGAGAA	GAAAGAGCAG	900
AAGAGTCAAT	TGAGGACATC	TATGCTAATA	TCCTGACCT	TCCAAAGTCC	TACATACCTT	960
CTAGGTTAAG	GAAGGAGATA	AATGAAGAAA	AAGAAGATGA	TGAACAAAAA	AGGAAAGCTT	1020
TATATGCCAT	GGAAATTTAA	GTTGAAAAAG	ACTTGAAGAC	TGGAGAAAGT	ACAGTTCTGT	1080
CTTCCAATAC	CTCTGGCCAT	CAGATGACTT	TAAAAGGTAC	AGGAGTAAAA	GTTTAAGATG	1140
ATGGGCAAAA	GTCCAGTGTA	TTCAGTAAAG	TGCTAATCAC	AAGTTGGAGG	TCAATGGCAT	1200
CGATGGCCTG	GCACCAAGTTG	AAGTAGAGGA	ACTTCTAAGA	CAAGCCTCAG	AGAGAAACTC	1260

TAAATCCCCA ACAGAGTATC ATGAGCCTGT ATATGCCAAT CCCTTTTACA GGCCTACAAC1320
 CCCACAGAGA GAAACGGTGA CCCCTGGACC AAACCTTTCAA GAAAGGATAA AGATTAAAAC1380
 TAATGGACTG GGTATTGGTG TAAATGAATC CATAACAAT ATGGGCAATG GTCTTTCAGA1440
 GGAAAGGGGA AACAACTTCA ATCACATCAG TCCCATTCCG CCAGTGCCTC ATCCCCGATC1500
 AGTGATTCAA CAAGCAGAAAG AGAAGCTTCA CACCCCGCAA AAAAGGCTAA TGAATCCTT31560
 GGAAGAATCG AATGTCATGC AGGACAAAGA TGCACCCTCT CCAAAGCCAA GGCTGAGCCC1620
 CAGAGAGACA ATATTTGGGA AATCTGAACA CCAGAATTCT TCACCCACTT GTCAGGAGGA1680
 CGAGGAAGAT GTCAGATATA ATATCGTTCA TTCCCTGCCT CCAGACATAA ATGATACAGA1740
 ACCGGTGACA ATGATTTTCA TGGGGTATCA GCAGGCAGAA GACAGTGAAG AAGATAAGAA1800
 GTTTCTGACA GGATATGATG GGATCATCCA TGCTGAGCTG GTTGTGATTG ATGATGAGGA1860
 GGAGGAGGAT GAAGGAGAAG CAGAGAAACC GTCCTACCAC CCCATAGCTC CCCATAGTCA1920
 GGTGTACCAG CCAGCCAAAC CAACACCACT TCCTAGAAAA AGATCAGAAG CTAGTCCTCA1980
 TGAAAACACA AATCATAAAT CCCCCACAA AAATTCCATA TCTCTGAAAG AGCAAGAAGA2040
 AAGCTTAGGC AGCCCTGTCC ACCATTCCCC ATTTGATGCT CAGACAACTG GAGATGGGAC2100
 TGAGGATCCA TCCTTAACAG CTTTAAGGAT GAGAATGGCA AAGCTGGGAA AAAAGGTGAT2160
 CTAAGAGTTG TACCACCTAT ATAAACATCC TTTGAAGAAG AAATAAGAA GCATTTGCAA2220
 ATTTCTCTTC TGGATATTTT GTTTATTTTT TCTGAAGTCC AAAAAATTAT CATTACAGTG2280
 TACCATATTA AGCCATGTGA ATAAGTAGTA GTCATTATTT GTGAAAAATT CCCAAAAAGC2340
 TGGGGAAAAC AAATGTGTAA CTTTCCAGT TACTTGACAC GATTCAAGTGG GGGAAAACCA2400
 GCATTTTTTA TTCTATTGAT ACCAAAGCAT TTCTAATAAG AGCTTGTTAA ATTTAAGAAT2460
 AAAGTTATTT AAAATATTCT GAGTATAGTA TATTAAGTGG CATTGTAATT TTGATGATAC2520
 AAAGATTGAA AGATCATAGG AAAGCATTGC CCTTCATCAC AGAAGTATTC AACTCTGACA2580
 AATAAATATG TCATCCTGAA TTAATAATGC CTTAATAAAA GTACATCCTC CTGCTAAAAA2640

(2) INFORMATION ON SEQ ID NO. 168:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1558 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260 69594960

GCGAGGAGCT GGCACGCAGC CAGGGCCTTT GCTCAAGAAG CCATACCAGC CAAGAATTAA 60
 AATCTCTAAA ACATCAGTGG ATGGTGATCC CCACTTTGTT GTGGATTTC CCCTGAGCAG 120
 ACTCACCGTG TGCTTCAACA TTGATGGGCA GCCCGGGGAC ATCCTCAGGC TGGTCTCTGA 180

(2) INFORMATION ON SEQ ID NO. 169:

(A) LENGTH: 1388 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

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CGGGGGTTCAC TGTGTTGGCC AGGCTGGTCT CGAACTCCTG ACCTCATGAT CTGCCCCGCCT 60
CAGCCTCCCA AAGTGCTGGG ATTACAAGTG TGAGCCACCA CACCTGGCCT GGAAGGAACC 120
TCTTAAAATC AGTTTACGTC TTGTATTTTG TTCTGTGATG GAGGACACTG GAGAGAGTTG 180

CTATTCCAGT CAATCATGTC GAGTCACTGG ACTCTGAAAA TCCTATTGGT TCCTTTATTT 240
TATTTGAGTT TAGAGTTCCC TTCTGGGTTT GTATTATGTC TGGCAAATGA CCTGGGTTAT 300
CACTTTTCCT CCAGGGTTAG ATCATAGATC TTGGAAACTC CTTAGAGAGC ATTTTGCTCC 360
TACCAAGGAT CAGATACTGG AGCCCCACAT AATAGATTTC ATTTCACTCT AGCCTACATA 420
GAGCTTTCTG TTGCTGTCTC TTGCCATGCA CTTGTGCGGT GATTACACAC TTGACAGTAC 480
CAGGAGACAA ATGACTTACA GATCCCCCGA CATGCCTCTT CCCCTTGGCA AGCTCAGTTG 540
CCCTGATAGT AGCACGTTTC TGTTTCTGAT GTACCTTTTT TCTCTTCTT TTTGCATCAG 600
CCAATTCCCA GAATTTCCCC AGGCAATTTG TAGAGGACCT TTTTGGGGTC CTATATGAGC 660
CATGTCCTCA AAGCTTTTAA ACCTCCTTGC TCTCCTACAA TATTCAGTAC ATGACCACTG 720
TCATCCTAGA AGGCTTCTGA AAAGAGGGGC AAGAGCCACT CTGCGCCACA AAGGTTGGGT 780
CCATCTTCTC TCCGAGGTTG TGAAAGTTTT CAAATTGTAC TAATAGGCTG GGGCCCTGAC 840
TTGGCTGTGG GCTTTGGGAG GGGTAAGCTG CTTTCTAGAT CTCTCCCAGT GAGGCATGGA 900
GGTGTTCCTG AATTTTGTCT ACCTCACAGG GATGTTGTGA GGCTTGAAAA GGTCAAAAAA 960
TGATGGCCCC TTGAGCTCTT TGTAAGAAAG GTAGATGAAA TATCGGATGT AATCTGAAAA1020
AAAGATAAAA TGTGACTTCC CTGCTCTGTG GCAGCAGTCG GGCTGGATGC TCTGTGGCCT1080
TTCTTGGGTC CTCATGCCAC CCCACAGCTC CAGGAACCTT GAAGCCAATC TGGGGGACTT1140
TCAGATGTTT GACAAAGAGG TACCAGGCAA ACTTCCTGCT ACACATGCCC TGAATGAATT1200
GCTAAATTTT AAAGGAAATG GACCCTGCTT TTAAGGATGT ACAAAGTAT GTCTGCATCG1260
ATGTCTGTAC TGTAATTTT TAATTTATCA CTGTACAAAG AAAACCCCTT GCTATTTAAT1320
TTTGTATTAA AGGAAAATAA AGTTTTGTTT GTTAAAAAAA AAAAAAAAAA AAAAAAAAAA1380
AAAAAAA

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(2) INFORMATION ON SEQ ID NO. 170:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2416 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

000260 "6954960

AAGAGGCCCG	TGGGGACACT	GTGCTGTTTT	GTTTCGTTTC	TGTGATCTCC	CGGCACGTTT	180
GGAGCTGGGA	AGACCACACT	GGTGGCAGAA	TCCTAAAATT	AAAGGAGGCA	GGCTCCTAGT	240
TGCTGAAAGT	TAAGGAATGT	GTAAAACCTC	CACGTGACTG	TTTGGTGCAT	CTTGACCTGG	300
GAAGACGCCT	CATGGGAACG	AACTTGGACA	GGTGTGGGT	TGAGGCCTCT	TCTGCAGGAA	360
GTCCCTGAGC	TGAGACGCAA	GTTGGCTGGG	TGGTCCACAC	CCTGGCTCTC	CTGCAGGTCC	420
ACACACCTTC	CAGGCCTGTG	GCCTGCCTCC	AAAGATGTGC	AAGGGCAGGC	TGGCTGCACG	480
GGGAGAGGGA	AGTATTTTGC	CGAAATATGA	GAACTGGGGC	CTCCTGCTCC	CAGGGAGCTC	540
CAGGGCCCCT	CTCTCCTCCC	ACCTGGACTT	GGGGGGAAC	GAGAAACACT	TTCTTGAGGC	600
TGCTGGCTTT	TGCACTTTTT	TGATGGCAGA	AGTGTGACCT	GAGAGTCCCA	CCTTCTCTTC	660
AGGAACGTAG	ATGTCGGGGT	GTCTTGCCCT	GGGGGGCTTG	GAACCTCTGA	AGGTGGGGAG	720
CGGAACACCT	GGCATCCTTC	CCCAGCACTT	GCATTACCGT	CCCTGCTCTT	CCCAGGTGGG	780
GACAGTGGCC	CAAGCAAGGC	CTCACTCGCA	GCCACTTCTT	CAAGAGCTGC	CTGCACACTG	840
TCTTGAGCA	TCTGCCTTGT	GCCTGGCACT	CTGCCGGTGC	CTTGGGAAGG	TCGGAAGAGT	900
GGACTTTGTC	CTGGCCTTCC	CTTCATGGCG	TCTATGACAC	TTTTGTGGTG	ATGGAAAGCA	960
TGGGACCTGT	CGTCTCAGCC	TGTTGGTTTT	TCCTCATTGC	CTCAAACCTT	GGGGTAGGTG	1020
GGACGGGGGG	TCTCGTGCCC	AGATGAAACC	ATTTGGAAAC	TCGGCAGCAG	AGTTTGTCCA	1080
AATGACCTTT	TTCAGGATGT	CTCAAAGCTT	GTGCCAAAGG	TCACTTTTCT	TTCTGCCTTT	1140
CTGCTGTGAG	CCCTGAGATC	CTCCTCCCAG	CTCAAGGGAC	AGGTCTTGGG	TGAGGGTGGG	1200
AGATTTAGAC	ACCTGAAACT	GGGCGTGGAG	AGAAGAGCCG	TTGCTGTTTG	TTTTTTGGGA	1260
AGAGCTTTTA	AAGAATGCAT	GTTTTTTTTT	TGGTTGGAAT	TGAGTAGGAA	CTTAGGGCTG	1320
GCTTCAGGTA	TGGTACAATC	AAGTGGGGGA	TTTTCATGCT	GAACCATTCA	AGCCCTCCCC	1380
GCCCCGTTGCA	CCCACTTTGG	CTGGCGTCTG	CTGGAGAGGA	TGCTCTGTCT	CGCATTCCCG	1440
TGCAGCTCCA	GGCTCGCGCA	GTTTTCTCTC	TCTCCCTGGA	TGTTGAGTCT	CATCAGAATA	1500
TGTGGGTAGG	GGGTGGACGT	GCACGGGTGC	ATGATTGTGC	TTAACTTGGT	TGTATTTTTT	1560
GATTTGACAT	GGAAAGCCTG	TTGCTTTGCT	CTTGAGAATA	GTTTCTCGTG	TCCCCCTCGC	1620
AGGCCTCATT	CTTTGAACAT	CAACTCTGAA	GTTTGATACA	GATAGGGGCT	TGATAGCTGT	1680
GGTCCCCCTC	CCCTCTGAC	TACCTAAAAT	CAATACCTAA	ATACAGAAGC	CTTGGTCTAA	1740
CACGGGACTT	TTAGTTTTCG	AAGGGCCTAG	ATAGGGAGAG	AGGTAACATG	AATCTGGACA	1800
GGGAGGGAGA	TACTATAGAA	AGGAGAACAC	TGCCTACTTT	GCAAGCCAGT	GACCTGCCTT	1860
TTGAGGGGAC	ATTGGACGGG	GGCCGGGGGC	GGGGGTGGG	TTTGAGCTAC	AGTCATGAAC	1920
TTTTGGCGTC	TACTGATTCC	TCCAACCTCT	CACCCCACAA	AATAACGGGG	ACCAATATTT	1980
TTAACTTTGC	CTATTTGTTT	TTGGGTGAGT	TTCCCCCTC	CTTATTCTGT	CCTGAGACCA	2040
CGGGCAAAGC	TCTTCATTTT	GAGAGAGAAG	AAAAACTGTT	TGGAACCACA	CCAATGATAT	2100
TTTTCTTTGT	AATACTTTGAA	ATTTATTTTT	TTATTATTTT	GATAGCAGAT	GTGCTATTTA	2160
TTTATTTTAAT	ATGATAAAGC	AGCCTAAACA	ATAGAAAGCT	GTAGAGATTG	GGTTTCATTG	2220
TTAATTGGTT	TGGGAGCCTC	CTATGTGTGA	CTTATGACTT	CTCTGTGTTT	TGTGTATTTG	2280
TCTGAATTAA	TGACCTGGGA	TATAAAGCTA	TGCTAGCTTT	CAACAGGAG	ATGCCTTTCA	2340
GAAATTTGTA	TATTTTGCAG	TTGCCAGACC	AATAAAATAC	CTGGTTGAAA	TACAAAAAAA	2400
AAAAAAAAAA	CTCGAG					2416

(2) INFORMATION ON SEQ ID NO. 171:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2720 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000260" 69554960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GGAGCTGTCC CTGACTNTGC AGGCCTGAGC GAGTGTGTGA GCATGCGGGG ACATGGGTGT 60
GTATGGCACA CATAGGTGCG TGTGTGTCTT TTGTATTTTT TCTCCTCCAA GGAGCTGTGT 120
CAGTGTGGAC GTTCTGTTTC AGGGAGTTGG AAAGGAGGGT GTCTGCAGAA GGTGGAGAGC 180
AGGGGCAGAG GCCCCACTGG CCACCCCTG CTTCCAGAG TGAAACCTTG TGCCTGGTGA 240
CCAAAGTCCC TCCAAAGTGC TCTTCCTTCT GGGTTATTCA AGCCAAATAT CTGGGTTTTCC 300
CCCTCTCCTC ATTCCCTAGC AAACCCCAAT TATCTTTCAA GATAGGAGAT ATTTCCCATC 360
CCCTTCCTTT GTAAATATCT CATCTCCCAC TGGAGAGCCC AGGAGCCTAT TCCTGGCATG 420
GATGTTCTGT CCACACTTGA GGCTGGGCGG TGTATCAGAC CCTTCAAGCA GCCTGGCTGG 480
GGCCAGGAC TGAGTCTGGG GTCAGCTTTC ACGGTCGCTT TTCCCTTCCT CACCACCCAC 540
CACAGCCCAC CTTGCATGCA TGGCCAGCCC CTCCACTCCA GCCTGAGCCA TGTGTGCCCC 600
TGCGGGAGGA CCCATTTCATG CCAGAAAGCT GGTAACCTCC TCCCAGCATC CCTGCGGAAG 660
GAGTCAGTTT CTGAGAGTGT GACTTTTCAA GGCGAATGAT GGGGAAGGGT TCCCCAGTCC 720
CCACAGTGGC CCCACCTCTG GGCCCTGCAC CAGAGCCCTT CTGTGTCACG GCGGGCTGTG 780
CACCCATGCA CACACCTACG CACACACAAC ACTCCGCACT GCAGTATATT CTTGCCAAAG 840
ATTTCTTTTA AAAGCAAGCA CTTTTACTAA TTATTATTTT GTAAATGTTT ATCTTCTTCT 900
GTCTTCTCCC TCCCTGAATC TATTTTACTG TTGTTTATTG TTGAATCTGT GTGTGAGCCA 960
GGAGAGCGCT GTCTGGCCTT GAACATGGGC TGGGATGGGA AAGGGTCTGG GAGAAGATGG1020
GCAACAAAGA GCCAGGGAGT CATGGACATC GCAGCGACGC AGACCCACAG AGGTTTCAGTC1080
CCGTGCTGCC ACCAGCTGTC CAGCTGGGTG TCTGGAGGGA AGAGGGCAGA GGAGGGTCAT1140
GTCCCTTCAG CTGGGGGAGG GGCCCACTGA GCTCCACGTG GCTTTTTCCC AAAGGGAGCA1200
AGAGGGAAGG ATTGCGCGAG AAAACAATGG AGAGGGGACC TGCGAAGGAA AACAGGGAGG1260
AAGTGAGCGG TTTGATCAGC CTGCTATCAC GGTGTTCTGG CTCTCTTATT TAGCCAGGCG1320
CTTAAGGGAC AGATACATCA CATCCTAAGT TTGGGAAAGG CCTTTGACCC ATGTCATCTG1380
AGCGTCTCCT CCAGTAGCTC TGAAAGCTGT GGACACCAAT GGCCAGGATT CCTTCTCCCC1440
TGTTTTTTGA GGATCCCTGG GTCTTCTGAG ACTGGCCAGG AGAGGGATGG TGGGGCCAGT1500
GCTTGTGTGA AAGCAGGAGG GGCAGCCCTC CTGGACAAGT GTGATCCCCC TATAACGGGC1560
TCTCAGGAGG TTAGTGAGTA GGAGATTCTG CCTTGTTCTG ATGAGCCTGT GCAGGGGCTC1620
CAGGGGAGCA TGCTGTCCAG GGGGCACAGA AGGGTGGTGA GTGTGATCAA ATCTAGTCTC1680
ACTCCCACTT TTTTAGTCTC ACTCCTACTT TTGTCCACCA CCCCTGCCTC CTGGATCTTC1740
TCCCACTTTT TTTTTCAGCT TTAGGACCTG GGGAGATCCT GTGAGTCAAG GCAGACACCC1800
AATCCTGCCC CCACACTCGG GGGTCCTCCC AAGAGGTTGG GGGGCAGAGT CCCAGAGCAG1860
CCCTTTACCC CAGGTCCAGG CCCTGGAATC CTGAGACTCG CGTTTCCTTG GCCAGTGGTA1920
ACACAGGACG TGTGTGCGCA TGTGCAAGTG TGGATGTATG TGTGTGCGTG TGTGTTGCTC1980
ATTTCTTTAG GGAACCTGGG AGTCGGGGTT GGAGGTGCTG GGCAATGGAA CTTCAAATTC2040
AATGTCGCCC AGCAGTGAGG GGAGTCGGGA GGTGAGGCCT GTAGGCCAAC CAATTGGTGG2100
AGTCTCAGCG ATAGCCCAGG TGAGAAGTGG TTCACCCAGA GGGGCAGGGT GGGGGCCTCG2160
GGCAGATCTG TCCCTCTTGG GCACCTCTGT CCTCAAATGT CCAAATGTT GGAGGACCTC2220
TGTTTCATATC CCACGCCTGG GCTCTTGCCA GCAGTGGAGT TACTGTAGAG GGATGTCCCA2280
AGCTTGTTTT CCAATCAGTG TTAAGCTGTT TGAAACTCTC CTGTGTCTGT GTTTTGTGTTG2340
TGCGTGTGTG TGAGAGCACA TCAGTGTGTG CAGGCTGTGT TTCCCCATTT CTCTCCTCCC2400
TTCAGACCCA TCATTGAGAA CAAATGTAAG AAATCCCTTC CCACCACCT CCCTGCCTCC2460
CAGGCCCTCT GCGGGGGAAA CAAGATCACC CAGCATCCTT CCCCACCCCA GCTGTGTATT2520

TATATAGATG GAAATATACT TTATATTTTG TATCATCGTG CCTATAGCCG CTGCCACCGT2580
GTATAAATCC TGGTGTCTGC TCCTTATCCT GGACATGAAT GTATTGTACA CTGACGCGTC2640
CCCACTCCTG TACAGCTGCT TTGTTTCTTT GCAATGCATT GTATGGCTTT ATAAATGATA2700
AAGTTAAAGA AAACCTCAAAA

(2) INFORMATION ON SEQ ID NO. 172:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2987 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

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CTCAATGCAG AGGATTTAAT CTAAAAGCAT ACAGAAATGC AGCTGAAATT GTGCAGTATG 60
GAGTAAAAAA TAACACCACT TTTCTGGAGT GTGCCCCCAA GTCTCCGCAG GCATCTATCA 120
AGTGGCTGTT ACAGAAAGAC AAAGACAGGA GGAAAGAGGT TAAGCTGAAT GAACGAATAA 180
TAGCCACTTC ACAGGGACTC CTGATCCGCT CTGTTTCAGGG TTCTGACCAA GGACTTTATC 240
ACTGCATTGC TACAGAAAAT AGTTTCAAGC AGACCATAGC CAAGATCAAC TTCAAAGTTT 300
TAGATTGAGA AATGGTGGCT GTTGTGACGG ACAAATGGTC CCCGTGGACC TGGGCCAGCT 360
CTGTGAGGGC TTTACCCCTT CACCCGAAGG ACATCATGGG GGCATTTCAGC CACTCAGAAA 420
TGCAGATGAT TAACCAATAC TGCAAAGACA CTCGGCAGCA ACATCAGCAG GGAGATGAAT 480
CACAGAAAAT GAGAGGGGAC TATGGCAAGT TAAAGGCCCT CATCAATAGT CGGAAAAGTA 540
GAAACAGGAG GAATCAGTTG CCAGAGTCAT AATATTTTCT TATGTGGGTC TTATGCTTCC 600
ATTAACAAAT GCTCTGTCTT CAATGATCAA ATTTTGAGCA AAGAACTTG TGCTTTACCA 660
AGGGGAATTA CTGAAAAAGG TGATTACTCC TGAAGTGAGT TTTACACGAA CTGAAATGAG 720
CATGCATTTT CTTGTATGAT AGTGACTAGC ACTAGACATG TCATGGTCCT CATGGTGCAT 780
ATAAATATAT TTAACCTAAC CCAGATTTTA TTTATATCTT TATTCACCTT TTCTTCAAAA 840
TCGATATGGT GGCTGCAAAA CTAGAATTGT TGCATCCCTC AATTGAATGA GGGCCATATC 900
CCTGTGGTAT TCCTTTCTCT CTTTGGGGCT TTAGAATTCT AATTGTCAGT GATTTTGTAT 960
ATGAAAACAA GTTCCAAATC CACAGCTTTT ACGTAGTAAA AGTCATAAAT GCATATGACA1020
GAATGGCTAT CAAAAGAAAT AGAAAAGGAA GACGGCATT TAAAGTTGTAT AAAACACGA1080
GTTATTCATA AAGAGAAAAT GATGAGTTTT TATGGTTCCA ATGAAATATG TTGGGGTTTT1140
TTTAAGATTG TAAAAATAAT CAGTTACTGG TATCTGTCAC TGACCTTTGT TTCCTTATTC1200

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096465569 "092000"

2987

(2) INFORMATION ON SEQ ID NO. 173:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 892 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

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TTTTTTCGGG AGGCAGAGTC TCCCTTTGTC GCCAGGCTGG AGTGCAGTGG TGCCATCTCG 60
GCTCACTGCA GCACTGTCTC GGCTCACTGC AGCCTCCGGC CTCCCGTATT CAAGCGATTG 120
TCCTGTCTCA GCCTCCTGAG TAGCTGGGAC TACAGGTGTG CACCACCACG CCCGGCTAAT 180
TTTTGTATTT TTAGTAGAGA CGGGGTTTCA CTGTGTTGGC CAGGATGGTC TCAATCTCGA 240
CCTCGTGATC CNCCCCACCT TGGCCTCCCA AAGTGTGGG ATTACAGGCN GTGACTCACC 300
ATGCCCAGCC ACTTAGTTTT TTCTTATTCC CACCTTTCTA TCCCATAGAA CACTCTTTTT 360
TATCTTCCCT GAACCANTAT TGNATGAGAT AAATANGGGC TGGGGGCTGG GNCCCCGCNT 420
GNGTCACNTC AACANGAGTN ATTTNCCCTT GGNCCGNAGA TNGGAAGTTT TGTNCCCAAT 480
ANGATGNAGC TGCTNGAGTA TCAACAAGGN TGACATTTTT CTGNCTGNCC CNATTTGTGT 540
CCTGGNNNAG ACNGGTNGGT ACCCTGAAGG NCAGANGGCC NAGCTGCCGC AAGACAGCAA 600
NTGACAGTCC ACCTGCCGAC CTGATTCTCTG CATCATGGAA TAANCCACNA TGGCTACCTT 660
CTATCCTCTG TTNCCCAAAT GGTGGNNTGG CACTTATCCT GAAGTCGTCN AATGATTTC 720
CTTTGNAAC TACTTTATTT TACTAATTTA AACTATTTTG TACTGATGTA GCCCTGAGGT 780
ANGTTCATGA AAATGCTGTG CACTCATTCC NATGGAATAA ATGTTGGAAA GCTGATCTTT 840
TCTGATATAA AATGTTGAAT GATANNAAAA AAAAAAAAAA AAAAAAAAAA AA 892

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(2) INFORMATION ON SEQ ID NO. 174:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1679 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

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GCACCCACTG GAAACACAGA CGGCACTCTG CGAAAGAGGA AGGGGCGCCA GGAGCTTGGA 60
TTAGAAAAC TGAAGCTTCAA GAACAGACTT GCCTAACAAAC AGGAAACTTG TATGTCTCGA 120

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09646569-092000

(2) INFORMATION ON SEQ ID NO. 175:

(A) LENGTH: 2411 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

TTCCAACGTT	CCCCTTGCCT	AAAATGTCCT	GGCAAACCAT	GGAAGCTTTG	ATGCAAGAAC	60
CCTGTTGTAC	TGGAGTTTTT	CTCCCCGTG	AAAAACGTAAC	TTACTGTTTG	GAGTGAATTG	120
AGGATGTAGA	AAGGGTGGTG	GAACCAAAAT	GTGGTCAATG	GAAATAGGAG	AATATGGTTC	180
TCACTCTTGA	GAaaaaaaACC	TAAGATTAGC	CCAGGTAGTT	GCCTGTAAct	TCAGTTTTTC	240
TGCCTGGGTT	TGATATAGTT	TAGGGTTGGG	GTTAGATTAA	GATCTAAATT	ACATCAGGAC	300
AAAGAGACAG	ACTATTAAct	CCACAGTTAA	TTAAGGACGT	ATGTTCCATG	TTTATTTGTT	360
AAAGCAGTGT	GAATAGCCTT	CAAGCATGTG	AATAATCTTC	CATCTTCCCC	GCCACACATA	420
CACACACACA	CTTTTTGTTT	CTTTCAGGTA	GACACCTTTT	AAAATGCAGA	ACTAACTGAG	480
GCATTTCACT	AACTTTGCTT	TCAAATCAAT	AAAGTCAAAT	GTATGGAAAC	ATTTTGTGCC	540
CTACTCTCCA	TACCCCGTGT	ACTCAAATTC	TCTACTGTAT	GAATTATGCT	TTAAGTAGAA	600
TTCACTGCCA	AGGAGAACTT	GGTGAAATAA	ATTATTTTAA	TTTTTTTTTTT	ATCCTTTTACA	660
AAGCCATGGA	TTTTATTTGG	TTGATGTGTG	CTCTGTACAC	AAGCCATTTC	AATAGGATGG	720
AGCTGTTAAT	TATTTTCCAA	AGAGTAATAG	ACATGCAAAA	GTTTCAATAA	AAACTGGGCC	780
ATTAACAAAT	AAATTAATAA	ACTAATAAGC	ATTCCCTTCT	AGGTTTTTGC	CAAACCTGCCT	840
ATCCAATAAC	AAATTTGAGA	ATCGTTGAAA	AAGCTAGTTA	TATTTCAAG	AAATGATTTT	900
CATTATTGAA	ACTGTTCTCC	CTAGCAGGCC	ATTTTCCCTT	TTTCCTGGGA	GTTTAGCAAG	960
TTTAGGAGAG	AATAGTCATG	AAAAGAAAGG	GAAGAAAGGG	GAGAAGGGAA	GAGGTTAAAA	1020
AGTAAGTGCT	CAGACCTATG	AACGTAATCC	CTTTGCTAGA	AATATTTAAG	AGCAGCTCAG	1080
CTTGGTTGAA	ACTGAGTTTT	GTCATCTTCC	ATATTGTCAG	GAAGGTATTT	TCTGACTTGC	1140
AATGCAGCTA	GATGTAAAAAT	TTTATTTTAT	CATACTAGAA	AGCCTTGACT	AGAAAAATGA	1200
ATAAATATTG	AGGGTTTCCT	GTCCATATCT	GGCTTGCATG	TGCCAGAAAG	CAGAGAAATAG	1260
AAAATGTAAT	CTCCAACATC	CAAGCATCGA	AACCCAAGGG	GTAGGCAATT	CTATGTAGGT	1320
TTTGACATG	AAGTTTGGTG	CATCTTGGTT	TATGCTGGCT	CAACTGCTAT	TAAACCTCTC	1380
TGGCTTATAG	TCTCTTCATT	CTATTAGACA	AGCACGTATC	GAACACTTGC	TTCGCACAAAG	1440
GCTCTTTAGT	TAACAATTTA	GCAGCTACTG	TTTGTGTTAA	ACACACTTTT	CACCAAATAG	1500
GTTCTGAGGC	AAACGAGAGC	AATGACTATT	TAAAGAAAGG	CTTTCCAGC	ATCACTTACA	1560
CATCCCAAAA	CTAAAAAGAT	CAACTCTTCC	AACCTGAGAA	AGACTCCTGG	CTTTGAATGG	1620
AAACTTACAG	CAGAGAGTCA	CAGGCCACGG	CAACAACAAC	GACAACAACA	AACATTTGGA	1680
ATATTATTCT	CAACTCACGT	TTTAATAATA	CATCTTATTA	TTTTTCTAGT	AGAGAAACTA	1740
CAAATCAGCC	TCTTCAACAT	TTATATACAG	TTTAATAAGC	CTCTTGCAAG	TTACTTGTTT	1800
TCTCACCTGA	GGTATTTTTT	TCCTCCCCAC	CTTGCCCCCT	TTCTCTCCTT	CCTCTTCTCC	1860
CTTTGCAAGA	GGAAATATTT	AACATATTTG	GGTCCAACCT	CAATAATGTA	ATAATTAATA	1920
CATTAAAAGC	ATTTAACTTC	CTTTCTAGAA	AAATGCACAG	GCTAAGGCAT	AGACAAAACA	1980
AAGAGAAATG	CTGAGAAATT	TGCCACTGGA	GACAAGCAAT	CTGAATAAAT	ATTTGCCAAA	2040
AGTTCTTTTT	ATGTCATATA	GTGTCAGGAT	TTGAAGGAGC	TATTTTTTTT	TAATGTTGCA	2100
ACTAGCAACT	CATCTTCGGA	AGACACAGCC	AGGAGAAATG	AGTAGAAGTG	AAAGGTTTAT	2160
AAATCCATTT	GTAAGCAATT	ATCCCATATA	TTTTAAATTC	AAGAAAAAAT	GTGTTTATCT	2220
TTAGAATTTT	GTATTCAATA	CTTTATGTAC	TATGTGACTC	ATGCTTCTGG	ATAAATAAAG	2280
CACCAAATAT	GTATCTGTAA	CCACAATCAC	ACATATTATA	TTAAATATAT	ATCTATATAA	2340
CAGCCAAAAA	AAAAAAAAAA	AAACACAAGA	AAAAGAAAGG	GAGAGGGGGG	GGGAGAGAAG	2400
GGGGGGGAGG	T					241

(2) INFORMATION ON SEQ ID NO. 176:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3450 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

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CTCGTCCCAAACCAGGACAC CCTCTCTACA GTAAATACAT GCGTGGGGAT GTACTTGTGA 60
TGCTGAAGCA GACGGAAAAT AATTACTTGG AGTGCCAAAA GGGAGAAGAC ACTGGCAGAG 120
TTCACCTGT( TCAAATGAAG ATTATCACTC CACTTGATGA ACATCTTAGA AGCAGACCAA 180
ACGATCCAA( CCACGCTCAG AAGCCTGTTG ACAGTGGTGC TCCTCATGCT GTCGTTCTTC 240
ATGATTTTCC( AGCAGAGCAA GTTGATGATT TGAACCTCAC TTCTGGAGAA ATTGGTTTAT 300
CTTCTGGAG AGATAGATAC AGATTGGTAC AGAGGGAAC GTAGAAACCA GATTGGCATA 360
TTTCCTGCC ACTATGTCAA AGTGATTATT GATATCCCAG AAGGAGGAAA TGGGAAAAGA 420
GAATGTGTT CATCTCATTG TGTAAAGGC TCAAGATGTG TTGCTCGGTT TGAATATATT 480
GGAGAGCAG AGGATGAGTT GAGTTTCTCA GAGGGAGAAA TTATTATTCT TAAAGAGTAT 540
GTGAATGAG AATGGGCCAG AGGAGAAGTT CGAGGCAGAA CTGGGATTTT CCCCCTGAAC 600
TTTGTGGA( CTGTTGAGGA TTATCCCACC TCTGGTGCAA ATGTTTTAAG CACAAAGGTA 660
CCACTGAA( CCAAAAAAGA AGATTCTGGC TCAAACTCTC AGGTTAACAG TCTTCCGGCA 720
GAATGGTG( AAGCTCTTCA CAGTTTTACA GCAGAGACCA GTGATGACTT ATCATTCAAG 780
AGGGGAGA( GGATCCAGAT TCTGGAACGT CTGGATTCTG ACTGGTGCAG GGGCAGACTG 840
CAGGACAG( AGGGGATCTT CCCAGCAGTG TTTGTGAGGC CCTGCCCAGC TGAGGCAAAA 900
AGTATGTT( CCATAGTACC GAAGGGGCAG GAAGGCCAAA GCCTTATATG ATTTCCGAGG 960
GGAGAATG( GATGAACTTT CCTTCAAGGC TGGAGATATA ATAACAGAGC TGGAATCTGT1020
AGATGATG( TGGATGAGTG GAGAACTTAT GGGAAAATCT GGAATATTTT CCAAAAACTA1080
CATACAGT( CTACAGATCA GCTAGAGGAG AAGCTTGTCT GTGTTCCCTT GCACAAGAAC1140
TCACTTGA( TATCACCTTG ACTATCAGAT ATGTTTTTGC ACTATTTTTT TTAAGTAAA1200
AAGAAATAC TAAGCTGTAC ATGGTACACT AGAATTTTCT GAAAGCAGAA AACGTTCA1260
TTTTGTAGT AATTTTCATT ACAATAGAAA CATGCACATG GAAACCCATG AGCTAGGATT1320
CTACCGAGA AAACATCTAG TGGGATTAGC AAGGTGAAGG GAAAGCATCT GGTGGCATGG1380
CAGCATGGG AGGCTCACAC ACAGAAGTTG CACGTGGACA TCTGTTTAA TCAGCACAAG1440
TGAATTAA( ATGCTTCTTC ATTTTTTTTAC TTTAGTTAAA AAAGAGGACA TTTAATATTC1500
TACATGCT( AACTATCAGG ACATGGTTAG CAATCTCAAT TTCATTTTTG ATATTCAAAT1560
TAATTCTT( AGCTTGAGCA TATCAGCCTT ATTACCAGAG CAAATCCTTC CTTCAGATGG1620
GATAGTTT( TGACTIONT GAGCATTTGT AAGCACATGG TGAAATCAGC CCCTGCCAC1680
CAAAATAA( TTTATGTTAC CAAGTGATTC CCATTTGTCT AAGGATTTGA AGGGGTCTA1740
AATTGGAT( ATCTTAGTCT AAAGAACCAA AACCATCCCT GAAATGCCTT GCTAATACAA1800
CTAATCCT( CATATATGTG CCATACTTAT TTTTTTCTC AGTGTATACT TTATGTTAAC1860
AGGGTTAT( CAAAGCACAT TTTCTGAATC TGCAATCATT CTTTGACAA TTAAGGACC1920
CAAAGGAAA( TTCATTTTCT TTGCATTATT CCAGTAATAT ATAAAACTG TGTCTTGT1980
TAGTAGTACA TTATGAATCA CATATAAAAT CTTACAATAC AGAACAAC TG TTAAGATGGA2040

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00226" 55594960

AAACAGTGCC AAACCTCCAC AGCTCATTTT TTTGTAATAT AATCAGAATG AAAAATAATT2100
 TAAGAGGACA GAAGACTGGT ACTTTTTTGT TTTATTTTTT CTCTAGCTTA TCCCTGCACA2160
 ATTATTAGAG TGAATGAAAA ACCACTTTCC TGCTTTCCAT TGTTATAAAT TCTAAGCTTA2220
 AGATAAAAGT GGTTCCTTTAC ATGACTGAAT CAATTACAAT TTATGGGCTA GAGCCAAATA2280
 GGTGAAGAC AATCATCCAA ACAGATCAAT GGAATAGAAT TTCATTGGAA ATGTAAAACA2340
 CTTTCCCAAC AATGGTCATG ACTTTCTTCT GTTTTGGAGA AGAGTTTCAT ATGCTGGACC2400
 ACATTTTAGC TTTTATTGTT TTTTTTTTCC CATTGTCCAA AAAGTTAAGC AACAAAGTGGC2460
 CACACTTTTA CGTGACTION ACCTGGAGTT CTGCAAAGAA GGTAATATTT ACTTGGTCTT2520
 TGACTIONAAGT TATCTCCCCA TTCTATGGTT ACATTTTATT TTGGACTATG GGGACTTCTA2580
 ATACGTTTTG GTAAAGAAGA GAGTATAAAG AAAATTCTTG TCAAATTTCA CTCAAAGTA2640
 ATTTTCATGAG AAATCAATGA TTTAAAGCAT TATCCAAATT AAATTATCAT TTGCAGCAA2700
 CTGTACAACA GCAGGAAGGA TATGGAATGG AACATGAGGT ATATATCTTT GCCTTTATAA2760
 TTTTAACATC TTATATTGAA GATTCTGAAA ACCTATCTTT ATTAGAGGAA AATCTCAATC2820
 TTCAGTTTTG GCCTTCTGTC ACCAGAATGA TAAGTGCAAT AGTTGTAAAT CTACTTGACA2880
 CTGTAATAAA CTGAACTGAA CTTTCAAAAT CCCTTTCTCA TACTAGACTG AGTTTTTTGA2940
 GAATGGAGGT GGAACCTTTT TTTTTTTTTT TTGTGAGACA GGATTAAATT CCCTTCGACC3000
 CAGGCTGGAG TGCAATGCAA TGTTGGCTCA CTGCAGCCTC TGCCTCCTGG GGCTCAAAGT3060
 GATTCTCCTG CCACAGCCTC CTGAGTAGCT GGGACTACAG GCGCACACCA CCCGTGCCCA3120
 GCTAATTTCT GGTATTTTTT TTTCTTTTGT TAGAGACAGG GTTTCGCCAT GTTGCCAGG3180
 CTGGGTTTCA AACACCTGGG CTCAAGCAGT CTGCCTGCCT CAGCCTCCCA AAGTGCTGGT3240
 AATACTGCAC CTGGGCCTGT GGTACCTTAT TTATCTTTGT ATCTCTAGTC CTTTGCACCA3300
 TTCAGCCTCA ATAAAGGTTG GTTGGTGGGT TGGGTGAGTT GGTGTTGG AATGGATGGA3360
 TGGATGGATG AATGACTTTC ACATACAGCA ATACCATCTT GGATTCACCT AATATCTTTC3420
 CTCTTTAATT TTTGACATAA ATCTATACTA 3450

(2) INFORMATION ON SEQ ID NO. 177:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 874 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

CGGGGGCGAG	CCGGGCCCTGC	GCGGTAGTGG	GACCCGACCC	TGCTCCAGT	GGGCGTCTTG	60
GGCCCCGGCT	CTATTCTGGG	CTGCGGCCCT	GGGAAGGGCT	CGCCGGGTGC	CAAATGAGCT	120
GTCTTAAGCT	TGCGGGGCTG	CAGCTTCCTG	CATGATGCTG	GGGAGCTTGG	CGCCTGACCC	180
AGGATCTAGA	AGGCACTCTG	GGCAGGCCGC	GCTCCGCCCA	CGAAGGTACC	CAACCTCTG	240
GGATAGATGC	AGGAAGCGAT	GGTTAAGACC	CATTTTCACC	CAACTTCTCG	CCGCAGTCTG	300
GCTTACCACA	CGCTCCTCCC	CATTCCCAGT	GAGCCGCTTT	TTGCAGCACC	AGGCGAACAC	360
TTACACCAGT	GCTTTGTAAA	GGAATCTTAT	TGTCCACCCC	GTGTCTTGGC	AAAAGAACAG	420
TGATCACACA	GATTCTACT	TGGGCTCTTT	CCTTTAATCT	TCGGAGGCTG	AGTTTGCCCA	480
ACTCAGGTTT	AACCACCAAG	GACTCTGAGA	GCTGGCAGGT	CTGAGTAACC	CTGGTAACAA	540
TTCTCTTCAC	CTTATCAAAA	CCTGAGCTAA	AACCAATGCA	TCAGCTGATG	ATGACAGCAG	600
AGAGTGGCAG	GGCTGAGGAC	CCAAAGTCAT	TTCCCAGGCT	GGCGGAGAAT	AAACTGCCAG	660
GGAGAAGAAT	GAGAAGACAG	GAGACAACT	GTTTGGAAG	CTAAATCTTC	CCTCTTAATG	720
AATAAAGGTT	TTTGCCTTGT	CTTAAAAAAT	AACAGGAAGA	AGCAGGGAAA	AATAAATAAC	780
TTATGGTAAT	CTGGAATTGT	ATTTTGTAAAT	ATTAAGTGTT	TTGAACCTCT	AACATTTACC	840
TTCCCCAAAA	ATCGAACCTT	CAGGTTTCAA	AAAT			874

(2) INFORMATION ON SEQ ID NO. 178:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3265 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

TACTTCTGCA	TGATGACAGA	AGCCGAGCAG	GACAAGTGGC	AGGCTGTGCT	GCAGGACTGC	60
ATCCGGCACT	GCAACAATGG	AATCCCTGAG	GACTCCAAGG	TAGAGGGCCC	TGCGTTTACA	120
GATGCCATCC	GCATGTACCG	ACAGTCCAAG	GAGCTGTACG	GCACCTGGGA	GATGCTGTGT	180
GGGAACGAGG	TGCAGATCCT	GAGCAACCTG	GTGATGGAGG	AGCTGGGCCC	TGAGCTGAAG	240
GCAGAGCTCG	GCCCCGCGCT	GAAGGGGAAA	CCGCAGGAGC	GGCAGCGGCA	GTGGATCCAG	300
ATCTCGGACG	CCGTGTACCA	CATGGTGTAC	GAGCAGGCCA	AGGCGCGCTT	CGAGGAGGTG	360
CTGTCCAAGG	TGCAGCAGGT	GCAGCCGGCC	ATGCAGGCCG	TCATCCGAAC	TGACATGGAC	420
CAAATTATCA	CCTCCAAGGA	GCACCTTGCC	AGCAAGATCC	GAGCCTTCAT	CCTCCCCAAG	480
GCAGAGGTGT	GCGTGC GGAA	CCATGTCCAG	CCCTACATCC	CATCCATCCT	GGAGGGCCCTG	540

ATGGTCCCCA CCAGCCAGGG CTTCACTGAG GTGCGAGATG TCTTCTTCAA GGAGGTCACG 600
 GACATGAACC TGAACGTCAT CAACGAGGGC GGCATTGACA AGCTGGGCGA GTACATGGAG 660
 AAGCTGTCCC GGCTGGCGTA CCACCCCTG AAGATGCAGA GCTGCTATGA GAAGATGGAG 720
 TCGCTGCGAC TGGACGGGCT GCAGCAGCGA TTTGATGTGT CCAGCACGTC CGTGTTCAAG 780
 CAGCGAGCCC AGATCCACAT GCGGGAGCAA ATGGACAATG CCGTGTATAC GTTCGAGACC 840
 CTCCTGCACC AGGAGCTGGG GAAGGGGCCC ACCAAGGAGG AGCTGTGCAA GTCCATCCAG 900
 CGGGTCCTGG AGCGGGTGCT GAAGAAATAC GACTACGACA GCAGCTCTGT GCGGAAGAGG 960
 TTCTTCCGGG AGGCGCTGCT GCAGATCAGC ATCCCGTTCC TGCTCAAGAA GCTGGCCCCCT1020
 ACCTGCAAGT CGGAGCTGCC CCGGTTCCAG GAGCTGATCT TCGAGGACTT TGCCAGGTTTC1080
 ATCCTGGTGG AAAACACGTA CGAGGAGGTG GTGCTGCAGA CCGTCATGAA GGACATCCTG1140
 CAGGCTGTGA AGGAGGCCGC GGTGCAGAGG AAGCACAACC TCTACCGGGA CAGCATGGTC1200
 ATGCACAACA GCGACCCCAA CCTGCACCTG CTGGCCGAGG GCGCCCCCAT CGACTGGGGC1260
 GAGGAGTACA GCAACAGCGG CGGGGGCGGC AGCCCAGCCC CAGCACCCCG GAGTCAGCCA1320
 CCCTCTCGGA AAAGCGACGG CGCGCCAAGC AGGTGGTCTC TGTGGTCCAG GATGAGGAGG1380
 TGGGGCTGCC CTTTGAGGTG AGCCCTGAGT CACCACCACC TGCGTCCCCG GACGGTGTCA1440
 CTGAGATCCG AGGCCTGCTG GCGCAAGGTC TGCGGCCTGA GAGCCCCCA CCAGCCGGCC1500
 CCCTGCTCAA CGGGGCCCCC GCTGGGGAGA GTCCCCAGCC TAAGGCCGCC CCCGAGGCCCT1560
 CCTCGCCGCC TGCCTCACCC CTCCAGCATC TCCTGCCTGG AAAGGCTGTG GACCTTGGGC1620
 CCCCCAAGCC CAGCGACCAG GAGACTGGAG AGCAGGTGTC CAGCCCCAGC AGCCACCCCG1680
 CCCTCCACAC CACCACCGAG GACAGTGCAG GGGTGCAGAC TGAGTTCTAG GCCAGTGGGT1740
 CCCTGACTGC TGCACATGGC ACAGGCCGTT CCCTTCCGGA CCCAGGCAGG CTCAGCTCTG1800
 GGGAGGGCAC CCTGGTCTGT GCCTTGTGGG TGGAGGCGGG GCAGGGCTGT GTGGCACC GC1860
 CAGGGAGCGG GCCCACCTGA GTCACCTTAT TGGGTTCACT CAACACTTTC TTGCTCCCTG1920
 TTTTCTCTTC TGTGGGATGA TCTCAGATGC AGGGGCTGGT TTTGGGGTTT TCCTGCTTGT1980
 GCCAAGGGCT GGACACTGCT GGGGGGCTGG AAAGCCCCTC CCTTCCTGTC CTTCTGTGGC2040
 CTCCATCCCC TCATGGGTGC TGCCATCCTT CCTGGAGAGA GGGAGGTGAA AGCTGGTGTG2100
 AGCCCAAGTGG GTTCCCGCCC ACTCACCCAG GAGCTGGCTG GGCCAGGACC GGGAGAGGGA2160
 GCACTGCTGC CCTCCTGGCC CTGCTCCTTC CGCAGTTAGG GGTGGACCGA GCCTCGCTTT2220
 CCCCCTGTT CTGGAGGGAA GGGGAAGGAG GGGGTCTTCA GGCTGGAGCC AGGCTGGGGG2280
 TGCTGGGTGG AGAGATGAGA TTTAGGGGGT GCCTCATGGG GTGGGCAGGC CTGGGGTGAA2340
 ATGAGAAAGG CCCAGAACGT GCAGGTCTGC GGAGGGGAAG TGTCCTGAGT GAAGGAGGGG2400
 ACCCCCATCC TGGGGGATGC TGGGAGTGAG TGAGTGAGTG AGATGGCTGA GTGAGGGTTA2460
 TGGGGAGCCT GAGGTTTTAT GGGCCTGTGT ATCCCCCTCT CCCGGCCCCA GCCTGCCTCC2520
 CTCCTGCCCC CCTGGCCAC AGGTCTCCCT CTGGTCCCTG TCCCTCTGGT GGTGGGGAT2580
 GGAGCGGCAG CAAGGGGTGT AATGGGGCTG GGTCTGTCT TCTACAGGCC ACCCCGAGGT2640
 CCTCAGTGGT TGCCTGGGGA GCCGACGGG GCTCCTGAGG GGTACAGGTT GGGTGGGCCC2700
 TCCCTGAGGG TCTGGGGTCA GGCTTTGGCC TCTGCTGCCT CTCAGTCACC AAGTCACCTC2760
 CCTCTGAAAA TCCAGTCCCT TCTTTGGATG TCCTTGTGAG TCACTCTGGG CCTGGCTGTC2820
 GTCCCTCCTC AGCTTCTTGT TCCTGGGACA AGGGTCAAGC CAGGATGGGC CCAGGCCTGG2880
 GATCCCCCAC CCCAGGACCC CCAGGCCCCC TCCCCTGCTG CTTTGCGGGG GGCAGGGCAG2940
 AAATGGACTC CTTTTGGGTC CCCGAGGTGG GGTCCCCTCC CAGCCCTGCA TCCTCCGTGC3000
 CGTAGACCTG CTCCCAGAG GAGGGGCCTT GACCCACAGG ACGTGTGGTG GCGCCTGGCA3060
 CTCAGGGACC CCCAGCTGCC CCAGCCCTGG TCTCTGGCGC ATCTCTTCCC TCTTGTCCCG3120
 AAGATCTGCG CCTCTAGTGC CTTTGTAGGG GTTCCCATCA TCCCTCCCTG ATATTGTATT3180
 GAAAAATATTA TGCACACTGT TCATGCTTCT ACTAATCAAT AAACGCTTTA TTAAAGCCA3240
 AAAAAAAG AGGGCGAAAA AAGGG

3265

(2) INFORMATION ON SEQ ID NO. 179:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 262 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

SLCVFPSSAA SFLSFLALVV AATMNKKKKP FLGMPAPLGY VPGLGRGATG FTTRSDIGPA 60
 RDANDPVDDR HAPPGKRTVG DQMKKNQAAD DDEDLNDTN YDEFNGYAGS LFSSGPLYEKD 120
 DEEADAIYAA LDKRMDERRK ERREQREKEE IEKYRMERPK IQQQFSDLKR KLAEVTEEEW 180
 LSIPEVG DAR NKRQRNPRYE KLTPVPDSFF AKHLOTGENH TSVDPRTQF GGLNTPYPGG 240
 LNTYPGGMT PGLMTPGTVS WT 262

(2) INFORMATION ON SEQ ID NO. 180:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 467 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

HTLSRWTKHS IPRWNDARTD DTWHSELDNR KIGQARNTLM DMRLSQVSDS VSGQTVVDPK 60
 GYLTDLNSMI PTHGGDINDI KKRLLLLKSV RETNPHHPPA WIASARLEEV TGKLQVARNL 120
 IMKGTEMCPK SEDVWLEAAR LQPGDTAKV VAQAVRHLPQ SVRIYIRAAE LETDIRAKKR 180
 VLRKALEHVP NSVRLWKAAR ELEEPEDARI MLSSRAVECCP TSVELWLALA RLETYENARK 240
 VLNKARENIP TDRHIWITAA KLEEANGNTQ MVEKIIDRAI TSLRANGVEI NREQWIQDAE 300
 ECDRAGSVAT CQAVMRAVIG IGIEEEDRKH TWMEDADSCV AHNALECARA IYAYALQVFP 360
 SKKSVWLRAA YFEKNHGTRE SLEALLQRAV AHCPKAEVLW LMGAKSKWLA GDVPAARSIL 420
 ALAFQANPNS EEIWLAAVKL ESENDEYERA RRLAKARTV PPPPGCS 467

(2) INFORMATION ON SEQ ID NO. 181:

009646569 "092000"

(A) LENGTH: 284 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

VRAGPEAAGQ	GADSAPTARV	FMKSVKLEWV	QDNIRAAQDL	CEEALRHYED	FPKLWMMKGQ	60
IEEQKEMMEK	AREAYNQGLK	KCPHSTPLWL	LLSRLEEKIG	QLTRARAILE	KSRLKNPKNP	120
GLWLESVRLE	YRAGLKNIAN	TLMAKALQEC	PNSGIDLWSEA	IFLEARPQRR	TKSVDALKKK	180
EHPDVLHLAV	AKLFWSQRKI	TKAREWFHRT	VKIDSDLGDA	WAFFYKFELQ	HGTEEQQEEV	240
RKRCESAEPR	HGELWCAVSK	DIANWQKKIG	DILRLVAGRI	KNTF		284

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 75 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

QPGIKESILM KETQGPYQGQ FLGQDSHQHI THVLLGREKQ YIPVERSQSI SGRNVVKGGR 60
CYAAAPSVPE VAVIP 75

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 75 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TFLLSLSYSS SRYFSQEFQR RLLKCLLAA QYQSINYPFW GLALEIIFVG RPNSSQQGSQ 60
ACLLDLFPLR GRNEL 75

(2) INFORMATION ON SEQ ID NO. 184:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 117 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

QGTRHPOSLS HKPAKKIDVA RVTFDLYKLN PQDFIGCLNV KATFYDTYSL SYDLHCCGAK 60
RIMKEAFRWA LFSMQATGHV LLGTSCYLQQ LLDATEEGQP PKGKASSLIP TCLKILQ 117

(2) INFORMATION ON SEQ ID NO. 185:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 143 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

KSAAQTAMTT PPQTPHPYF INRQDFPCIL LRISSSHSPA PSPMSWLHHC KTDLLQGSQK 60
LLLALYHFYP HLPPEATATIH SHCPSALRPS SRADGSMVIL SWVVLLKPSQ GADSQRASRV 120
SGLDDSKEGT PIFIFKTDIP RGF 143

000260-092000

(2) INFORMATION ON SEQ ID NO. 186:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

TQTRHFQLAT QSGRAGGNTD LDIHKKIKPK IKHSILCPLK GLIKGTQSPP RSPLPCQHHK 60
ASSAHTKGLG RGILLPPHQP QEWT 84

(2) INFORMATION ON SEQ ID NO. 187:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

RHWGFTASIF SLKRFITSTS KEQTNWRNVC FFFLFIKFYS TAKFQISFTY RPCKGTVRTE 60
HLFYLRDQGV EIFSLNFIRK GWVQWLMPVI SAFWEAEAGR SLVARSLRPA WATQ 114

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

000260"69594960

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

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NLINKKKKKHT FLQLVCSLLV EVINRFKEKI LAVNPOCLQL FWQNIFKEIQ QANFEVLMKV 60
KEGGISSFGR NEKCLTRDIT THVSGSCFLP KTFREEVN                               98

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(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

KYELYTENAT	TEKTEPNSEQ	DKNDGGKSRK	GNIELASSEP	QHFTTTVTRC	SPTVAFVEFP	60
SSPQLKNDVS	EEKDQKKPEN	EMSGKVELVL	SQKVVKPKSP	EPEATLTFFP	LDKMPEANQL	120
HLPNLNSQVD	SPSSEKSPVM	TPFKFWAWDP	EEERRRQEKW	QQEQERLLQE	RYQKEQDKLK	180
EEWEKAQKEV	EEEERRYYEE	ERKIIEDTVV	PFTVSSSSAD	QLSTSSSMTE	GSGMTNKKIDL	240
GNCQDEKQDR	RWKKSFOGDD	SDLLLKTRES	DRLEEKGSLT	EGALAHSGNP	VSKGVHEDHQ	300
LDTEAGAPHC	GTNPQLAQDP	SQNQOTSNTPT	HSSDEVKPKT	LPLDKSINHQ	IESPSERRKS	360
ISGKKLCSSC	GLPLGKGAAM	IIETLNLVYH	IQCFRCGICK	GQLGDAVSGT	DVRIRNGLLN	420
CNDCYMRSRS	AGQPTTL					437

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

SANHKLEVNG	TDGLAPVEVE	ELLRQASERN	SKSPTEYHEP	VYANPFYRPT	TPQRETVTPG	60
PNFQERIKIK	TNGLGIGVNE	SIHNMGNGLS	EERGNNFNHI	SPIPPVPHPR	SVIQQAAEKL	120
HTPQKRLMTP	WEESNVMQDK	DAPSPKPRLS	PRETIFGKSE	HQNSSPTCQE	DEEDVRYNIV	180
HSLPPDINDT	EPVTMIFMGY	QQAEDSEEDK	KFLTGYDGII	HAELVVIDDE	EEEDEGEAEK	240
PSYHPIAPHS	QVYQPAKPTP	LPRKRSEASP	HENTNHKSPH	KNSISLKEQE	ESLGSPVHHS	300
PFDQOTTGDG	TEDPSLTALR	MRMAKLGGKV	I			330

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 216 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

LSLTSRMEEA	ELVKGRLLQAI	TDKRKIQEEI	SQKRLKIEED	KLKHQHLKKK	ALREKWLLDG	60
ISSGKEQEEM	KKQNQQDQHQ	IQVLEQSILR	LEKEIQDLEK	AELQISTKEE	AILKKLKSIE	120
RTTEDIIRSV	KVEREERAEF	SIEDIYANIP	DLPKSYIPSR	LRKEINEEKE	DDEQNRKALY	180
AMEIKVEKDL	KTGESTVLSS	NTSGHQMTLK	GTGVKV			216

(2) INFORMATION ON SEQ ID NO. 192:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 290 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

RGAGTQPGPL LKKPYQPRIK ISKTSVDGDP HFVVDFFPLSR LTVCFNIDGQ PGDILRLVSD 60
HRDSGVTVNG ELIGAPAPPN GHKKQRTYLR TITILINKPE RSYLEITPSR VILDGGDRLV 120
LPCNQSVVVG SWGLEVSVSA NANVTVTIQG SIAFVILIHL YKKPAPFQRH HLGFIYANSE 180
GLSSNCHGLL GQFLNQDARL TEDPAGPSQN LTHPLLLQVG EGPEAVLTVK GHQVPVVWKQ 240

RKIYNGEEQI DCWFARNNA KLIDGEYKDY LASHPFDTGM TLGQGMSREL 290

(2) INFORMATION ON SEQ ID NO. 193:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 87 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

GHGSYRTPKR SSTNCLGKFW ELADAKKKRK KVHQKQKRAT IRATELAKGK RHVGGSVSHL 60
SPGTVKCVIT AQVHGKRQQQ KALCRLE 87

(2) INFORMATION ON SEQ ID NO. 194:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 82 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

QFIQGMCSRK FAWYLFVKHL KVPQIGFKVP GAVGWHDPR KATEHPARLL HRAGEVTFYL 60
FFRLHPIFHL PFLQRAQGAI IF 82

000260"65594960

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 251 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```

DDRSFHFHHH KSVIDAMKGR PGQSPLFRPS QGTGRVPGTR QMLQDSVQAA LEEVAASEAL 60
LGPLSPPGKS RDGNASAGEG CQVFRSPPSE VSPPPGQDTP TSTFLKRRWD SQVTLLPSKK 120
CKSQQLQESV SQFPSPGGR REGPWSSLGA GGPSSHISAK YFPLPVQPAC PCTSLEAGHR 180
PGRCVDLQES QGVDHPANLR LSSGTSCRRG LNPTPVQVRS HEASSQVKMH QTVTWRFYTF 240
LNFAQLGACL L 251

```

(2) INFORMATION ON SEQ ID NO. 196:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

FAKGLDRERG NMNLDREGDT IERRTLPTLQ ASDLPFEGTL DGGRGRGLGL SYSHELLAST 60
DSSNSPPHKI TGTNIFNFAY LFLGEFPPSL FCPETTCKAL HFEREEKLFG TTPMIFFFVI 120
LEIYFFIILI ADVLFIYLIC IRSNNRKL 149

```

(2) INFORMATION ON SEQ ID NO. 197:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein

000260" 69594960

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```
GQRCPRGTDL PEAPTLPLWV NHFSPGLSLR LHQLVGLQAS PPDSPHCWAT LNLKFHCPAP 60
PTPTPKFPKE MSKTHAHTYI HTCTCAHTSC VTTGQGNASL RIPGPGPGVK GCSGTLPPNL 120
LGGPPSVGAG LGVCLDSQDL PRS 143
```

(2) INFORMATION ON SEQ ID NO. 198:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 142 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```
SHTMHCKETK QLYRSGDASV YNTFMSRIRS RHQDLYTVAA AIGTMIQNIK YISIVINTQL 60
GWGRMLGDLV SPAEGLGGRE GGGKGFLTFV LNDGSEGRRE MGKHSLSLTM CSHTHAQTKH 120
RHRRVSNLSLT LIGKQAWDIP LQ 142
```

(2) INFORMATION ON SEQ ID NO. 199:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 189 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

000250" 6954960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

QCRGFNLKAY RNAAEIVQYG VKNNTTFLEC APKSPQASIK WLLQKDKDRR KEVKLNERII 60
 ATSQGLLIRS VQGSQGLYH CIATENSFKQ TIAKINFKVL DSEMVAVVD KWSPWTWASS 120
 VRALPFHPKD IMGAFSHSEM QMINQYCKDT RQQHQQGDDES QKMRGDYGKL KALINSRKSR 180
 NRRNQLPES 189

(2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 97 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

FFREAESPFV ARLECSGAIS AHCSTVSAHC SLRPPVFKRF SCLSLSSWD YRCAPPRPAN 60
 FCIFSRDGVLS LCWPGWSQSR PRDPAHLGLP KCWDYRX 97

(2) INFORMATION ON SEQ ID NO. 201:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 250 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

0000260"69594960

(2) INFORMATION ON SEO ID NO. 202:

- EKTPGFEWKL TAESHRPRQQ QRQQOTFGIL FSTHVLIIHL IIFLVEKLQI SLFNIYIQFN 60
KPLASYLFSL LRYFFPPHLA PVPPFLFSLC KRKYLTYLGP TSIM 104

(2) INFORMATION ON SEQ ID NO. 203:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 93 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```

HKKNFWQIFI QIACLQWQIS QHFSLFCLCL SLCIFLERKL NAFNVLIITL LKLDPNMLNI 60
SSCKGRRGRE EOGQGEEKN TSGERTSNLO EAY 93

```

(2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

RPKPGHPLYL KYMRGDVLVM LKQTENNYLE CQKGEDTGRV HLSQMKIITP LDEHLRSRPN 60
 DPSHAQKPVD SGAPHAVVLH DFPAEQVDDL NLTSGEIGLS SGEDRYRLVQ REL 113

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 225 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

TSLLEKLVYL LEKIDTDWYR GNCRNQIGIF PANYVKVIID IPEGGNGKRE CVSSHCVKGS 60
 RCVARFEYIG EQKDELSFSE GEIIILKEYV NEEWARGEVR GRTGIFPLNF VEPVEDYPTS 120
 GANVLSTKVP LKTKKEDSGS NSQVNSLP AE WCEALHSFTA ETSDDLSEFKR GDRIQILERL 180
 DSDWCRGRLQ DREGIFPAVF VRPCPAEAKS MLAIVPKGQE GQSLI 225

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

000250" 69594960

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CIGFSSGFDK VKRIVTRVTQ TCQLSESLVV KPELGKLSLR RLKERAQVGI CVITVLLPRH 60
 GVDNKIPLQS TGVSVRLVLQ KAAHWEWGGA CGKPDCEKL GENGS 105

(2) INFORMATION ON SEQ ID NO. 207:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

LCGAAASCMM LGSLAPDPGS RRHSGQAALR PRRYPTLWDR CRKRWLRPIF TQLLAHVWLT 60
 TRSSFPFVSR FLQHQAQNTYT SAL 83

(2) INFORMATION ON SEQ ID NO. 208:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 581 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

000260" 69594950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

YFCMMTEAEQ	DKWQAVLQDC	IRHCNNGIPE	DSKVEGPAFT	DAIRMYRQSK	ELYGTWEMLC	60
GNEVQILSNL	VMEELGPELK	AELGPRLK GK	PQERQROWIQ	ISDAVYHVMV	EQAKARFEEV	120
LSKVQQVQPA	MQAVIRTDMD	QIITSKEHLA	SKIRAFILPK	AEVCVRNVHQ	PYIPSILEAL	180
MVPTSQGFTE	VRDVFFKEVT	DMNLNVINEG	GIDKLGEYME	KLSRLAYHPL	KMQSCYEKME	240
SLRLDGLQQR	FDVSSTSVFK	QRAQIHMREQ	MDNAVYTFET	LLHQELGKGP	TKEELCKSIQ	300
RVLERVLLKKY	DYDSSSVRKR	FFREALLOIS	IPFLLLKKLAP	TCKSELPRFQ	ELIFEDFARF	360
ILVENTYEEV	VLQTVMKDIL	QAVKEAAVQR	KHNLYRDSMV	MHNSDPNLHL	LAEGAPIDWG	420
EEYSNSGGGG	SPAPAPRSQP	PSRKS DGAPS	RWSLWSRMRR	WGCPRLRLALS	HHHLRPRTVS	480
LRSEACWPKV	CGLRAPHQPA	PCSTGPPLGR	VPSLRPPPRP	PRRLPHPSSI	SCLERLWTLG	540
PPSPATRRL E	SRCPAPAATP	PSTPPPRTVQ	GCRLSSRPVG	P		581

(2) INFORMATION ON SEQ ID NO. 209:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 466 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

PQRAAPPPHP	GPQRPPAWRA	VAFPRGWLTP	GCWGWAAAPA	AVAVLLAPVD	GGALGQQVQV	60
GVAVVHDHAV	PVEVVLPLHR	GLLHSLQDVL	HDGLQHLLLV	RVFHQDEPGK	VLEDQLLEPG	120
QLRLAGRGQL	LEQERDADLQ	QRLPEEPLPH	RAAVVVVFLQ	HPLQDPLDGL	AQLLLGGPLP	180
QLLVQEGLER	IHGIVHLLPH	VDLGSLLHGG	RAGHIKSLLO	PVQSQRLLHL	IAALHLQGVV	240
RQPQQLLHVL	AQLVNAALVD	DVQVHVRDLL	EEDISHLSEA	LAGGDHQGLQ	DGWDVGLDMV	300
PHAHLCLGED	EGSDLAGKVL	LGGDNLVHVS	SDDGLHGRLH	LLHLGQHLLLE	ARLGLLVHHV	360
VHGVRDLPL	PLPLRRFPLQ	PRAELCLQLR	AQLLHHQVAQ	DLHLVPTQHL	PGAVQLLGLS	420
VHADGICERR	ALYLGVLGRS	IVAVPDAVLO	HSLPLVLLGF	CHHAEV		466

WO 99/47655

PCT/DE99/00909

Claims

1. A nucleic acid sequence that codes a gene product or a part thereof, comprising

a) a nucleic acid sequence, selected from the group Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178

b) an allelic variation of the nucleic acid sequences named under a)

or

c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID No. 178, characterized in that it is expressed elevated in normal breast tissue.

4. BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID No. 178, for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

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7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 6.

9. A nucleic acid sequence according to claims 1 to 7,
wherein the size of the fragment has a length of at least 150 to
4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

24. Polypeptide partial sequences according to claim 22,
with at least 90% homology to these sequences.

32. A nucleic acid sequence according to claims 1 to 10,
wherein it is an mRNA sequence.

33. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID NO. 161 to Seq. ID No. 178.

34. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

35. Use according to claim 34, wherein the regulatory element is a suitable promoter and/or enhancer.

36. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

37. The nucleic acid sequences Seq. ID No.: 3, 37, 45, wherein they are associated with lipometabolism and can be used for treatment of pathological alterations of the lipometabolism.

09646569 092000

DECLARATION FOR PATENT APPLICATION

51572

As a below named inventor, I hereby declare that

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original first and sole inventor (if only one name is listed below) or an original first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 19 MARCH 1999 as United States Application Number or PCT International Application Number PCT/DE99/00909 and (if applicable) was amended on _____

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification including the claims as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.36

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate or PCT International application having a filing date before that of the application on which priority is claimed

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119

APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 13 835.0	GERMANY	20/03/98	YES

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)

APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120

APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E. J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brian P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lepovitz (37,067); John H. Thomas (33,460); Catherine M. Joyce (40,668); Nancy J. Axelrod (44,014); James T. Moore (35,619); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

Correspondence Address:

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Arlington, VA 22201

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Declaration for Patent Application (Continued)

51572

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

-00	Full Name of sole or first inventor (given name family name)	
	Thomas SPECHT	
	Signature <i>Thomas Specht</i>	Date <i>16.08.00</i>
	Residence <i>DEX</i>	Citizenship German
	Post Office Address Grabenstrasse 14, D-12209 Berlin, Germany	
2-00	Full Name of additional joint inventor (given name family name)	
	Bernd HINZMANN	
	Signature <i>Bernd Hinzmann</i>	Date <i>17.08.00</i>
	Residence <i>DEX</i>	Citizenship German
	Post Office Address Parkstrasse 19, D-13127 Berlin, Germany	
3-00	Full Name of additional joint inventor (given name family name)	
	Armin SCHMITT	
	Signature <i>Armin Schmitt</i>	Date <i>September 4, 2000</i>
	Residence <i>DEX</i>	Citizenship German
	Post Office Address Laubacher Strasse 6/II, D-14197 Berlin, Germany	
4-00	Full Name of additional joint inventor (given name family name)	
	Christian PILARSKY	
	Signature <i>Christian Pilarsky</i>	Date <i>10.08.00</i>
	Residence <i>DEX</i>	Citizenship German
	Post Office Address Heinrich-Lange-Strasse 13c, D-01474 Schönfeld, Germany	
5-00	Full Name of additional joint inventor (given name family name)	
	Edgar DAHL	
	Signature <i>Edgar Dahl</i>	Date <i>10.08.2000</i>
	Residence <i>DEX</i>	Citizenship German
	Post Office Address Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany	
6-00	Full Name of additional joint inventor (given name family name)	
	André ROSENTHAL	
	Signature <i>André Rosenthal</i>	Date <i>29/8/00</i>
	Residence <i>DEX</i>	Citizenship German
	Post Office Address Koppenplatz 10, D-10115 Berlin, Germany	

□ Additional joint inventors are named on separately numbered sheets attached hereto

DECLARATION FOR PATENT APPLICATION

51572

As a below named inventor, I hereby declare that

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 19 MARCH 1999 as United States Application Number or PCT International Application Number PCT/DE99/00909 and (if applicable) was amended on

I hereby authorize our attorneys to insert the serial number assigned to this application

I hereby state that I have reviewed and understand the contents of the above-identified specification including the claims as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States listed below and have also identified below, by checking the box any foreign application for patent or inventor's certificate or PCT International application having a filing date before that of the application on which priority is claimed

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119

APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 13 835.0	GERMANY	20/03/98	YES

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)

APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120

APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E. J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brion P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebowitz (37,067); John H. Thomas (33,460); Catherine M. Joyce (40,668); Nancy J. Axelrod (44,014); James T. Moore (35,619); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

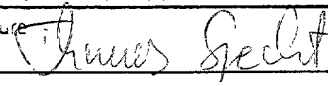
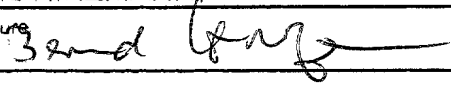


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Declaration for Patent Application (Continued)

515-2

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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☐ Additional joint inventors are named on separately numbered sheets attached hereto

Sequence protocol

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<210> 18

<211> 1722

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1722

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<212> DNA
<213> homo sapiens

<400> 19

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<210> 21
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<212> DNA
<213> homo sapiens

<400> 21

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<400> 22
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<210> 41

<211> 2939

<212> DNA

<213> homo sapiens

<400> 41

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<211> 3670

<212> DNA

<213> homo sapiens

<400> 42

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3670

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 <213> homo sapiens

<400> 43

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<210> 45
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<212> DNA
<213> homo sapiens
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gatggcacaa	ctgtatagag	agaagagtag	tccaagccc	tggcagggga	tacagtgttc	480
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<210> 46
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<210> 47
<211> 360
<212> DNA
<213> homo sapiens
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<211> 2192
<212> DNA
<213> homo sapiens
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<210> 49
<211> 2952
<212> DNA
<213> homo sapiens
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<212> DNA
<213> homo sapiens

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<212> DNA
<213> homo sapiens

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<210> 53
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 <212> DNA
 <213> homo sapiens

<400> 53

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 <211> 1301
 <212> DNA
 <213> homo sapiens

<400> 54

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<400> 55

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<210> 56

<211> 1265

<212> DNA

<213> homo sapiens

<400> 56

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<211> 274

<212> DNA

<213> homo sapiens

<400> 57

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<212> DNA
<213> homo sapiens

<400> 58

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<211> 850
<212> DNA
<213> homo sapiens

<400> 59

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 <211> 2952
 <212> DNA
 <213> homo sapiens

<400> 61

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<212> DNA

<213> homo sapiens

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<210> 68
 <211> 2403
 <212> DNA
 <213> homo sapiens

<400> 68

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<210> 69
<211> 1246
<212> DNA
<213> homo sapiens
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<210> 71
<211> 1950
<212> DNA
<213> homo sapiens
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<210> 72
 <211> 814
 <212> DNA
 <213> homo sapiens

<400> 72

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<210> 74
 <211> 747
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<400> 74

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<210> 76
<211> 2419
<212> DNA
<213> homo sapiens

<400> 76

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<211> 366
<212> PRT
<213> homo sapiens

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<400> 77

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Val	Trp	Leu 35	Glu	Ala	Ala	Arg	Leu 40	Gln	Pro	Gly	Asp	Thr 45	Ala	Lys	Ala
Val	Val 50	Ala	Gln	Ala	Val	Arg 55	His	Leu	Pro	Gln	Ser 60	Val	Arg	Ile	Tyr
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Leu	Arg	Lys	Ala	Leu 85	Glu	His	Val	Pro	Asn 90	Ser	Val	Arg	Leu	Trp 95	Lys
Ala	Ala	Val	Glu 100	Leu	Glu	Glu	Pro	Glu 105	Asp	Ala	Arg	Ile	Met 110	Leu	Ser
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Gln	Trp	Ile 195	Gln	Asp	Ala	Glu	Glu 200	Cys	Asp	Arg	Ala	Gly 205	Ser	Val	Ala
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Glu 225	Asp	Arg	Lys	His	Thr 230	Trp	Met	Glu	Asp	Ala 235	Asp	Ser	Cys	Val	Ala 240
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 <211> 25
 <212> PRT
 <213> homo sapiens

<400> 80

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			20					25							

<210> 81
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 <212> PRT
 <213> homo sapiens

<400> 81

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			20					25							

<210> 82
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 <212> PRT
 <213> homo sapiens

<400> 82

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			20					25					30		

<210> 83
 <211> 54
 <212> PRT
 <213> homo sapiens

<400> 83

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Glu	Lys	Gln	Tyr	Ile	Pro	Val	Glu	Arg	Ser	Gln	Ser	Ile	Ser	Gly	Arg
			20					25					30		
Asn	Val	Val	Lys	Gly	Gly	Arg	Cys	Tyr	Ala	Ala	Ala	Pro	Ser	Val	Pro
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<210> 84
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 <212> PRT
 <213> homo sapiens

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<400> 84

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Asp	Glu	Lys 35	Lys	Val	Ala	Leu	Leu 40	Tyr	Leu	Asp	Asn	Glu 45	Glu	Glu	Glu
Asn	Asp 50	Gly	His	Trp	Phe										

<210> 85

<211> 116

<212> PRT

<213> homo sapiens

<400> 85

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Phe	Ile	Gly 35	Cys	Leu	Asn	Val	Lys 40	Ala	Thr	Phe	Tyr	Asp 45	Thr	Tyr	Ser
Leu	Ser 50	Tyr	Asp	Leu	His	Cys 55	Cys	Gly	Ala	Lys	Arg 60	Ile	Met	Lys	Glu
Ala 65	Phe	Arg	Trp	Ala	Leu 70	Phe	Ser	Met	Gln	Ala 75	Thr	Gly	His	Val	Leu 80
Leu	Gly	Thr	Ser	Cys 85	Tyr	Leu	Gln	Gln	Leu 90	Leu	Asp	Ala	Thr	Glu 95	Glu
Gly	Gln	Pro	Pro 100	Lys	Gly	Lys	Ala	Ser 105	Ser	Leu	Ile	Pro	Thr 110	Cys	Leu
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<210> 86

<400> 86

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<210> 87

<211> 71

<212> PRT

<213> homo sapiens

<400> 87

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95

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His	Ala	Asp 35	Leu	Cys	Gln	Leu	Cys 40	Leu	Leu	Ala	Lys	Cys 45	Phe	Lys	Pro
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Gly 65	Ala	Tyr	Asp	Ala	Lys 70	His	Phe	Leu	Cys	Tyr 75	Tyr	Tyr	Tyr	Gly	Gly 80
Met	Ile	Tyr	Thr	Gly 85	Leu	Lys	Asn	Phe	Glu 90	Arg	Ala	Leu	Tyr	Phe 95	Tyr
Glu	Gln	Ala	Ile 100	Thr	Thr	Pro	Ala	Met 105	Ala	Val	Ser	His	Ile 110	Met	Leu
Glu	Ser	Tyr 115	Lys	Lys	Tyr	Ile	Leu 120	Val	Ser	Leu	Ile	Leu 125	Leu	Gly	Lys
Val	Gln 130	Gln	Leu	Pro	Lys	Tyr 135	Thr	Ser	Gln	Ile	Val 140	Gly	Arg	Phe	Ile
Lys 145	Pro	Leu	Ser	Asn	Ala 150	Tyr	His	Glu	Leu	Ala 155	Gln	Val	Tyr	Ser	Thr 160
Asn	Asn	Pro	Ser	Glu 165	Leu	Arg	Asn	Leu	Val 170	Asn	Lys	His	Ser	Glu 175	Thr

Phe Thr Arg Asp 180 Asn Asn Met Gly Leu 185 Val Lys Gln Cys Leu 190 Ser Ser

Leu Tyr Lys 195 Lys Asn Ile Gln Arg 200 Leu Thr Lys Thr Phe 205 Leu Thr Leu

Ser Leu 210 Gln Asp Met Ala Ser 215 Arg Val Gln Leu Ser 220 Gly Pro Gln Glu

Ala 225 Glu Lys Tyr Val Leu 230 His Met Ile Glu Asp 235 Gly Glu Ile Phe Ala 240

Ser Ile Asn Gln Lys 245 Asp Gly Met Val Ser 250 Phe His Asp Asn 255 Pro Glu

Lys Tyr Asn Asn 260 Pro Ala Met Leu His 265 Asn Ile Asp Gln Glu 270 Met Leu

Lys Cys Ile 275 Glu Leu Asp Glu Arg 280 Leu Lys Ala Met Asp 285 Gln Glu Ile

Thr Val 290 Asn Pro Gln Phe Val 295 Gln Lys Ser Met Gly 300 Ser Gln Glu Asp

Asp 305 Ser Gly Asn Lys Pro 310 Ser Ser Tyr Ser

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<211> 58

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<213> homo sapiens

<400> 91

Val 1 Leu Gln Glu Lys 5 Ile Lys Ile Lys Lys 10 Glu Lys Lys Glu Lys 15 Ile

Lys Phe Lys Asn 20 Cys Phe Glu Asn Val 25 Gln Ile Lys Ser Asn 30 Ile Leu

Ile Ile His 35 Leu His Val Leu Leu 40 Asn Ile Leu Ile Met 45 Trp Met Phe

Thr Leu 50 Cys Met Ile Leu Ala 55 Glu Tyr His

<210> 92

<211> 201

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<213> homo sapiens

<400> 92

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000269" 69294960

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	50					55					60					
Leu	Ser	Pro	Arg	Glu	Thr	Ile	Phe	Gly	Lys	Ser	Glu	His	Gln	Asn	Ser	
65					70					75					80	
Ser	Pro	Thr	Cys	Gln	Glu	Asp	Glu	Glu	Asp	Val	Arg	Tyr	Asn	Ile	Val	
				85					90					95		
His	Ser	Leu	Pro	Pro	Asp	Ile	Asn	Asp	Thr	Glu	Pro	Val	Thr	Met	Ile	
			100					105					110			
Phe	Met	Gly	Tyr	Gln	Gln	Ala	Glu	Asp	Ser	Glu	Glu	Asp	Lys	Lys	Phe	
		115					120					125				
Leu	Thr	Gly	Tyr	Asp	Gly	Ile	Ile	His	Ala	Glu	Leu	Val	Val	Ile	Asp	
	130					135					140					
Asp	Glu	Glu	Glu	Glu	Asp	Glu	Gly	Glu	Ala	Glu	Lys	Pro	Ser	Tyr	His	
145					150					155					160	
Pro	Ile	Ala	Pro	His	Ser	Gln	Val	Tyr	Gln	Pro	Ala	Lys	Pro	Thr	Pro	
				165					170					175		
Leu	Pro	Arg	Lys	Arg	Ser	Glu	Ala	Ser	Pro	His	Glu	Asn	Thr	Asn	His	
			180					185					190			
Lys	Ser	Pro	His	Lys	Asn	Ser	Ile	Ser	Leu	Lys	Glu	Gln	Glu	Glu	Ser	
		195					200					205				
Leu	Gly	Ser	Pro	Val	His	His	Ser	Pro	Phe	Asp	Ala	Gln	Thr	Thr	Gly	
	210					215					220					
Asp	Gly	Thr	Glu	Asp	Pro	Ser	Leu	Thr	Ala	Leu	Arg	Met	Arg	Met	Ala	
225					230					235					240	
Lys	Leu	Gly	Lys	Lys	Val	Ile										
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Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	Ser	Lys	Asn	Gly	Ser	Gly	Asn
			20					25					30		
Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met
		35					40					45			
Pro	Gly	Lys	Asn	Ala	Val	Thr	Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys
	50					55					60				
Leu	Ala	Leu	Arg	His	Gly	Ala	Asp	Leu	Val	Pro	Ile	Tyr	Ser	Phe	Gly
65					70					75					80
Glu	Asn	Glu	Val	Tyr	Lys	Gln	Val	Ile	Phe	Glu	Glu	Gly	Ser	Trp	Gly
				85					90					95	
Arg	Trp	Val	Gln	Lys	Lys	Phe	Gln	Lys	Tyr	Ile	Gly	Phe	Ala	Pro	Cys
			100					105					110		
Ile	Phe	His	Gly	Arg	Gly	Leu	Phe	Ser	Ser	Asp	Thr	Trp	Gly	Leu	Val
		115					120					125			
Pro	Tyr	Ser	Lys	Pro	Ile	Thr	Thr	Val	Val	Gly	Glu	Pro	Ile	Thr	Ile
	130					135					140				
Pro	Lys	Leu	Glu	His	Pro	Thr	Gln	Gln	Asp	Ile	Asp	Leu	Tyr	His	Thr
145					150					155					160
Met	Tyr	Met	Glu	Ala	Leu	Val	Lys	Leu	Phe	Asp	Lys	His	Lys	Thr	Lys
				165					170					175	
Phe	Gly	Leu	Pro	Glu	Thr	Glu	Val	Leu	Glu	Val	Asn				
			180					185							

<210> 96
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<400> 96

Arg	Gly	Ala	Gly	Thr	Gln	Pro	Gly	Pro	Leu	Leu	Lys	Lys	Pro	Tyr	Gln
1				5					10					15	
Pro	Arg	Ile	Lys	Ile	Ser	Lys	Thr	Ser	Val	Asp	Gly	Asp	Pro	His	Phe
			20					25					30		
Val	Val	Asp	Phe	Pro	Leu	Ser	Arg	Leu	Thr	Val	Cys	Phe	Asn	Ile	Asp
		35					40					45			
Gly	Gln	Pro	Gly	Asp	Ile	Leu	Arg	Leu	Val	Ser	Asp	His	Arg	Asp	Ser

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50					55					60					
Gly 65	Val	Thr	Val	Asn	Gly 70	Glu	Leu	Ile	Gly	Ala 75	Pro	Ala	Pro	Pro	Asn 80
Gly	His	Lys	Lys	Gln 85	Arg	Thr	Tyr	Leu	Arg 90	Thr	Ile	Thr	Ile	Leu 95	Ile
Asn	Lys	Pro	Glu 100	Arg	Ser	Tyr	Leu	Glu 105	Ile	Thr	Pro	Ser	Arg 110	Val	Ile
Leu	Asp	Gly 115	Gly	Asp	Arg	Leu	Val 120	Leu	Pro	Cys	Asn	Gln 125	Ser	Val	Val
Val	Gly 130	Ser	Trp	Gly	Leu	Glu 135	Val	Ser	Val	Ser	Ala 140	Asn	Ala	Asn	Val
Thr 145	Val	Thr	Ile	Gln	Gly 150	Ser	Ile	Ala	Phe	Val 155	Ile	Leu	Ile	His	Leu 160
Tyr	Lys	Lys	Pro	Ala 165	Pro	Phe	Gln	Arg	His 170	His	Leu	Gly	Phe	Tyr 175	Ile
Ala	Asn	Ser	Glu 180	Gly	Leu	Ser	Ser	Asn 185	Cys	His	Gly	Leu	Leu 190	Gly	Gln
Phe	Leu	Asn 195	Gln	Asp	Ala	Arg	Leu 200	Thr	Glu	Asp	Pro	Ala 205	Gly	Pro	Ser
Gln	Asn 210	Leu	Thr	His	Pro	Leu 215	Leu	Leu	Gln	Val	Gly 220	Glu	Gly	Pro	Glu
Ala 225	Val	Leu	Thr	Val	Lys 230	Gly	His	Gln	Val	Pro 235	Val	Val	Trp	Lys	Gln 240
Arg	Lys	Ile	Tyr	Asn 245	Gly	Glu	Glu	Gln	Ile 250	Asp	Cys	Trp	Phe	Ala 255	Arg
Asn	Asn	Ala	Ala 260	Lys	Leu	Ile	Asp	Gly 265	Glu	Tyr	Lys	Asp	Tyr 270	Leu	Ala
Ser	His	Pro 275	Phe	Asp	Thr	Gly	Met 280	Thr	Leu	Gly	Gln	Gly 285	Met	Ser	Arg
Glu	Leu 290														

<210> 97
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<213> homo sapiens

<400> 97

Asn	Gln	Phe	Thr	Ser	Cys	Ile	Leu	Phe	Cys	Asp	Gly	Gly	His	Trp	Arg	
1				5					10					15		
Glu	Leu	Leu	Phe	Gln	Ser	Ile	Met	Ser	Ser	His	Trp	Thr	Leu	Lys	Ile	
			20					25					30			
Leu	Leu	Val	Pro	Leu	Phe	Tyr	Leu	Ser	Leu	Glu	Phe	Pro	Ser	Gly	Phe	
		35					40					45				
Val	Leu	Cys	Leu	Ala	Asn	Asp	Leu	Gly	Tyr	His	Phe	Ser	Ser	Arg	Val	
	50					55					60					
Arg	Ser															
65																

<210> 98

<211> 54

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<400> 98

Val	Pro	Gly	Ala	Leu	Pro	Leu	Ala	Val	Gly	Pro	Pro	Pro	Pro	Pro	Ser	
1				5					10					15		
Gly	Phe	Pro	Arg	Asn	Val	Gln	Pro	Arg	Arg	Pro	Ser	Gln	Ser	Leu	Gly	
		20						25				30				
Arg	Val	Met	Ser	Ala	Gly	Pro	Asp	Lys	Arg	Pro	Leu	Gly	Thr	Leu	Cys	
		35					40					45				
Cys	Phe	Val	Ser	Phe	Leu											
	50															

<210> 99

<211> 49

<212> PRT

<213> homo sapiens

<400> 99

Phe	Phe	Leu	Tyr	Phe	Asn	Gln	Val	Phe	Tyr	Trp	Ser	Gly	Asn	Cys	Lys	
1				5					10					15		
Ile	Tyr	Lys	Phe	Leu	Lys	Gly	Ile	Ser	Cys	Leu	Lys	Ala	Ser	Ile	Ala	
		20						25				30				
Leu	Tyr	Pro	Arg	Ser	Leu	Ile	Gln	Thr	Asn	Thr	Gln	Asn	Thr	Glu	Lys	
		35					40					45				

Ser

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<400> 100

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<213> homo sapiens
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Trp	Thr	Ser	Gln 20	Arg	Arg	Arg	Pro	Gln 25	Gln	Val	Gln	Ser	Arg 30	Ala	Ala
Thr	Ser	Cys 35	Pro	Ala	Gly	Cys	Leu 40	Glu	Gly	Arg	Gly	Gln 45	Arg	Arg	Val
Met	Ser 50	Leu	Gln	Leu	Gly	Glu 55	Gly	Pro	Ser	Glu	Leu 60	His	Val	Ala	Phe
Ser 65	Gln	Arg	Glu	Gln	Glu 70	Gly	Arg	Ile	Gly	Arg 75	Glu	Asn	Asn	Gly	Glu 80
Gly	Thr	Cys	Glu	Gly 85	Lys	Gln	Gly	Gly	Ser 90	Glu	Arg	Phe	Asp	Gln 95	Pro
Ala	Ile	Thr	Val 100	Phe	Trp	Leu	Ser	Tyr 105	Leu	Ala	Arg	Arg	Leu 110	Arg	Asp

Pro
145

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<210> 103
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<400> 103

Met 1	Arg	Thr	His	Val 5	Leu	Cys	Tyr	His	Trp 10	Pro	Arg	Lys	Arg	Glu 15	Ser
Gln	Asp	Ser	Arg 20	Ala	Trp	Thr	Trp	Gly 25	Lys	Gly	Leu	Leu	Trp 30	Asp	Ser
Ala	Pro	Gln	Pro	Leu	Gly	Gly	Pro	Arg	Val	Trp	Gly	Gln	Asp	Trp	Val

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							54								
		35					40					45			
Ser	Ala	Leu	Thr	His	Arg	Ile	Ser	Pro	Gly	Pro	Lys	Ala	Glu	Lys	Lys
	50					55					60				
Ser	Gly	Arg	Arg	Ser	Arg	Arg	Gln	Gly	Trp	Trp	Thr	Lys	Val	Gly	Val
65					70				75						80
Arg	Leu	Lys	Ser	Gly	Ser	Glu	Thr	Arg	Phe	Asp	His	Thr	His	His	Pro
				85					90					95	
Ser	Val	Pro	Pro	Gly	Gln	His	Ala	Pro	Leu	Glu	Pro	Leu	His	Arg	Leu
			100					105					110		
Ile	Arg	Thr	Arg	Gln	Asn	Leu	Leu	Leu	Thr	Asn	Leu	Leu	Arg	Ala	Val
		115					120					125			
Tyr	Arg	Gly	Ile	Thr	Leu	Val	Gln	Glu	Gly	Cys	Pro	Ser	Cys	Phe	His
	130					135					140				
Thr	Thr	Thr	Gly	Pro	Thr	Ile	Pro	Leu	Leu	Ala	Ser	Leu	Arg	Arg	Pro
145					150					155					160
Arg	Asp	Pro	Gln	Lys	Pro	Gly	Glu	Lys	Glu	Ser	Trp	Pro	Leu	Val	Ser
				165					170					175	
Thr	Ala	Phe	Arg	Ala	Thr	Gly	Gly	Asp	Ala	Gln	Met	Thr	Trp	Val	Lys
			180					185					190		
Gly	Leu	Ser	Gln	Thr											
		195													

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<400> 104

Ser	Glu	Ala	Arg	Asn	Ala	Pro	Ser	Gly	Thr	Ala	Gln	Thr	Phe	Ala	Met
1				5					10					15	
Gly	Phe	Met	Thr	Gly	Thr	Ile	Ser	Ser	Met	Tyr	Gln	Thr	Lys	Ala	Val
			20					25					30		
Ile	Ile	Ala	Met	Ile	Ile	Thr	Ala	Val	Val	Ser	Ile	Ser	Val	Thr	Ile
		35					40					45			
Phe	Cys	Phe	Gln	Thr	Lys	Val	Asp	Phe	Thr	Ser	Cys	Thr	Gly	Leu	Phe
	50					55					60				
Cys	Val	Leu	Gly	Ile	Val	Leu	Leu	Val	Thr	Gly	Ile	Val	Thr	Ser	Ile

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65						70			55							80
Val	Leu	Tyr	Phe	Gln 85	Tyr	Val	Tyr	Trp	Leu 90	His	Met	Leu	Tyr	Ala 95	Ala	
Leu	Gly	Ala	Ile 100	Cys	Phe	Thr	Leu	Phe 105	Leu	Ala	Tyr	Asp	Thr 110	Gln	Leu	
Val	Leu	Gly 115	Asn	Arg	Lys	His	Thr 120	Ile	Ser	Pro	Glu	Asp 125	Tyr	Ile	Thr	
Gly	Ala 130	Leu	Gln	Ile	Tyr	Thr 135	Asp	Ile	Ile	Tyr	Ile 140	Phe	Thr	Phe	Val	
Leu 145	Gln	Leu	Met	Gly	Asp 150	Arg	Asn									

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His 1	Leu	Leu	Ser	Pro 5	Pro	His	Ile	Leu	Gly 10	Thr	Ala	Phe	Ser	Ser 15	Thr
Gly	Asn	Gly	Thr 20	Asp	Gly	Gln	Lys	Thr 25	Ser	Ile	Thr	Phe	Met 30	Lys	Gly
Leu	Leu	Glu 35	Leu	Pro	Gly	Lys	Lys 40	Ala	Cys	Leu	Gly	Glu 45	Leu	Gly	Arg
Cys	Arg 50	Gln	Cys	Gly	Trp	Ala 55	Gly	Gly	Gln	Pro	Val 60	Val	Leu	Leu	Pro
Ala 65	Gln														

<210> 106
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<400> 106

Pro 1	Thr	Ser	Leu	Ile 5	Trp	Pro	Thr	Thr	Met 10	Phe	Cys	Ser	Val	His 15	Val
Leu	Phe	Lys	Ser 20	Ile	Leu	Asn	Trp	Leu 25	Pro	Ser	Phe	Lys	Leu 30	Asn	Gln
Thr	Leu	Lys 35	Ala	Trp	Ser	Ser	His 40	Thr	Gly	Pro	Thr	Phe 45	Pro	His	Gly

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Asn	Tyr	Glu	Arg	Ala	Pro	Ala	Gln	Gln	Gly	Leu	Ser	Arg	Ser	Leu	Pro
	50					55	56				60				
Pro	Pro	Leu	Pro	Val	Pro	Gln	Ile	Trp	Pro	Leu	Leu	Arg	Lys	Ile	Arg
65					70					75					80
Thr	Ala	Thr	Gly	Pro	Ser	Glu	Pro	Lys	Pro	Thr					
				85					90						

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<400> 107

Leu	Leu	Pro	Ser	Phe	Phe	Leu	His	Phe	Ser	Leu	Ser	Ile	Tyr	Phe	Pro
1				5					10					15	
His	Pro	Thr	Phe	Leu	Glu	Gln	Pro	Leu	Val	Leu	Gln	Glu	Met	Ala	Leu
			20					25					30		
Met	Asp	Arg	Arg	Leu	Ala	Leu	Pro	Ser							
		35					40								

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<400> 108

Asn	Glu	Leu	Lys	Ala	Ser	Gly	Gly	Glu	Ile	Lys	Ile	His	Lys	Met	Glu
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Gln	Lys	Glu	Asn	Val	Pro	Pro	Gly	Pro	Glu	Val	Cys	Ile	Thr	His	Gln
			20					25					30		
Glu	Gly	Glu	Lys	Ile	Ser	Ala	Asn	Glu	Asn	Ser	Leu	Ala	Val	Arg	Ser
		35					40					45			
Thr	Pro	Ala	Glu	Asp	Asp	Ser	Arg	Asp	Ser	Gln	Val	Lys	Ser	Glu	Val
	50					55					60				
Gln	Gln	Pro	Val	His	Pro	Lys	Pro	Leu	Ser	Pro	Asp	Ser	Arg	Ala	Ser
65					70					75					80
Ser	Leu	Ser	Glu	Ser	Ser	Pro	Pro	Lys	Ala	Met	Lys	Lys	Phe	Gln	Ala
				85					90					95	
Pro	Ala	Arg	Glu	Thr	Cys	Val	Glu	Cys	Gln	Lys	Thr	Val	Tyr	Pro	Met
			100					105					110		
Glu	Arg	Leu	Leu	Ala	Asn	Gln	Gln	Val	Phe	His	Ile	Ser	Cys	Phe	Arg
		115					120					125			

Cys	Ser 130	Tyr	Cys	Asn	Asn	Lys 135	Leu	Ser	Leu	Gly	Thr 140	Tyr	Ala	Ser	Leu
His 145	Gly	Arg	Ile	Tyr	Cys 150	Lys	Pro	His	Phe	Asn 155	Gln	Leu	Phe	Lys	Ser 160
Lys	Gly	Asn	Tyr	Asp 165	Glu	Gly	Phe	Gly	His 170	Arg	Pro	His	Lys	Asp 175	Leu
Trp	Ala	Ser	Lys 180	Asn	Glu	Asn	Glu	Glu 185	Ile	Leu	Glu	Arg	Pro 190	Ala	Gln
Leu	Ala	Asn 195	Ala	Arg	Glu	Thr	Pro 200	His	Ser	Pro	Gly	Val 205	Glu	Asp	Ala
Pro	Ile 210	Ala	Lys	Gly	Gly	Val 215	Leu	Ala	Ala	Ser	Met 220	Glu	Ala	Lys	Ala
Ser 225	Ser	Gln	Gln	Glu	Lys 230	Glu	Asp	Lys	Pro	Ala 235	Glu	Thr	Lys	Lys	Leu 240
Arg	Ile	Ala	Trp	Pro 245	Pro	Pro	Thr	Glu	Leu 250	Gly	Ser	Ser	Gly	Ser 255	Ala
Leu	Glu	Glu	Gly 260	Ile	Lys	Met	Ser	Lys 265	Pro	Lys	Trp	Pro	Pro 270	Glu	Asp
Glu	Ile	Ser 275	Lys	Pro	Glu	Val	Pro 280	Glu	Asp	Val	Asp	Leu 285	Asp	Leu	Lys
Lys	Leu 290	Arg	Arg	Ser	Ser	Ser 295	Leu	Lys	Glu	Arg	Ser 300	Arg	Pro	Phe	Thr
Val 305	Ala	Ala	Ser	Phe	Gln 310	Ser	Thr	Ser	Val	Lys 315	Ser	Pro	Lys	Thr	Val 320
Ser	Pro	Pro	Ile	Arg 325	Lys	Gly	Trp	Ser	Met 330	Ser	Glu	Gln	Ser	Glu 335	Glu
Ser	Val	Gly	Gly 340	Arg	Val	Ala	Glu	Arg 345	Lys	Gln	Val	Glu	Asn 350	Ala	Lys
Ala	Ser	Lys 355	Lys	Asn	Gly	Asn	Val 360	Gly	Lys	Thr	Thr	Trp 365	Gln	Asn	Lys
Glu	Ser 370	Lys	Gly	Glu	Thr	Gly 375	Lys	Arg	Ser	Lys	Glu 380	Gly	His	Ser	Leu

Glu Met Glu Asn Glu Asn Leu Val⁵⁸ Glu Asn Gly Ala Asp Ser Asp Glu
 385 390 395 400
 Asp Asp Asn Ser Phe Leu Lys Gln Gln Ser Pro Gln Glu Pro Lys Ser
 405 410 415
 Leu Asn Trp Ser Ser Phe Val Asp Asn Thr Phe Ala Glu Glu Phe Thr
 420 425 430
 Thr Gln Asn Gln Lys Ser Gln Asp Val Glu Leu Trp Glu Gly Glu Val
 435 440 445
 Val Lys Glu Leu Ser Val Glu Glu Gln Ile Lys Arg Asn Arg Tyr Tyr
 450 455 460

Asp Glu Asp Glu Asp Glu Glu
 465 470

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<210> 112
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 <212> PRT
 <213> homo sapiens

<400> 112

Arg Lys Met Leu Arg Ala Ala Leu Pro Ala Leu Pro Ile Pro Arg Cys
 1 5 10 15
 Lys Tyr Thr Leu Phe Leu Ile Ala His Met Gly Pro Pro Tyr Leu Leu
 20 25 30
 Ala Leu Val Leu Met Leu Lys Ser Trp Pro Trp Glu Arg Cys Leu Pro
 35 40 45
 Gly Arg His Ser Cys Leu Val Gln Ala Lys Pro Leu Cys Asn Ala Ser
 50 55 60
 Pro Phe Trp Cys Tyr Glu Val Pro Leu Cys Arg Arg Phe His Gln Gln
 65 70 75 80
 Leu Val Thr Val Pro Ser Thr Arg Thr Cys Phe Glu Ile Ser
 85 90

<210> 113

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Gly 1	Leu	Ser	Thr	Phe 5	Gln	Asn	Trp	Leu	Pro 10	Ser	Thr	Pro	Ala	Thr 15	Ser	
Trp	Gly	Gly	Leu 20	Thr	Ser	Ser	Arg	Thr 25	Thr	Asp	Asn	Gly	Gly 30	Glu	Gln	
Thr	Ala	Leu 35	Ser	Pro	Gln	Glu	Ala 40	Pro	Phe	Ser	Gly	Ile 45	Ser	Thr	Pro	
Pro	Asp 50	Val	Leu	Ser	Val	Gly 55	Pro	Glu	Pro	Ala	Trp 60	Glu	Ala	Ala	Ala	
Thr 65	Thr	Lys	Gly	Leu	Ala 70	Thr	Asp	Val	Ala	Thr 75	Phe	Thr	Gln	Gly	Ala 80	
Ala	Pro	Gly	Arg	Glu 85	Asp	Thr	Gly	Leu	Leu 90	Thr	Thr	Thr	His	Gly 95	Pro	
Glu	Glu	Ala	Pro 100	Arg	Leu	Ala	Met	Leu 105	Gln	Asn	Glu	Leu	Glu 110	Gly	Leu	
Gly	Asp	Ile 115	Phe	His	Pro	Met	Asn 120	Ala	Glu	Glu	Gln	Ala 125	Gln	Leu	Ala	
Ala	Ser 130	Gln	Pro	Gly	Pro	Lys 135	Val	Leu	Ser	Ala	Glu 140	Gln	Gly	Ser	Tyr	
Phe 145	Val	Arg	Leu	Gly	Asp 150	Leu	Gly	Pro	Ser	Phe 155	Arg	Gln	Arg	Ala	Phe 160	
Glu	His	Ala	Val	Ser 165	His	Leu	Gln	His	Gly 170	Gln	Phe	Gln	Ala	Arg 175	Asp	
Thr	Leu	Ala	Gln 180	Leu	Gln	Asp	Cys	Phe 185	Arg	Leu	Ile	Glu	Lys 190	Ala	Gln	
Gln	Ala	Pro 195	Glu	Gly	Gln	Pro	Arg 200	Leu	Asp	Gln	Gly	Ser 205	Gly	Ala	Ser	
Ala	Glu 210	Asp	Ala	Ala	Val	Gln 215	Glu	Glu	Arg	Asp	Ala 220	Gly	Val	Leu	Ser	
Arg 225	Val	Cys	Gly	Leu	Leu 230	Arg	Gln	Leu	His	Thr 235	Ala	Tyr	Ser	Gly	Leu 240	

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Val	Ser	Ser	Leu	Gln 245	Gly	Leu	Pro ⁶⁰	Ala	Glu 250	Leu	Gln	Gln	Pro	Val 255	Gly
Arg	Ala	Arg	His 260	Ser	Leu	Cys	Glu	Leu 265	Tyr	Gly	Ile	Val	Ala 270	Ser	Ala
Gly	Ser	Val 275	Glu	Glu	Leu	Pro	Ala 280	Glu	Arg	Leu	Val	Gln 285	Ser	Arg	Glu
Gly	Val 290	His	Gln	Ala	Trp	Gln 295	Gly	Leu	Glu	Gln	Leu 300	Leu	Glu	Gly	Leu
Gln 305	His	Asn	Pro	Pro	Leu 310	Ser	Trp	Leu	Val	Gly 315	Pro	Phe	Ala	Leu	Pro 320

Ala Gly Gly Gln

<210> 114
 <211> 148
 <212> PRT
 <213> homo sapiens

<400> 114

Ile 1	Ala	Met	Thr	Pro 5	Pro	Asn	Ala	Thr	Glu 10	Ala	Ser	Lys	Pro	Gln 15	Gly
Thr	Thr	Val	Cys 20	Pro	Pro	Cys	Asp	Asn 25	Glu	Leu	Lys	Ser	Glu 30	Ala	Ile
Ile	Glu	His 35	Leu	Cys	Ala	Ser	Glu 40	Phe	Ala	Leu	Arg	Met 45	Lys	Ile	Lys
Glu	Val 50	Lys	Lys	Glu	Asn	Gly 55	Asp	Lys	Lys	Ile	Val 60	Pro	Lys	Lys	Lys
Lys 65	Pro	Leu	Lys	Leu	Gly 70	Pro	Ile	Lys	Lys	Lys 75	Asp	Leu	Lys	Lys	Leu 80
Val	Leu	Tyr	Leu	Lys 85	Asn	Gly	Ala	Asp	Cys 90	Pro	Cys	His	Gln	Leu 95	Asp
Asn	Leu	Ser	His 100	His	Phe	Leu	Ile	Met 105	Gly	Arg	Lys	Val	Lys 110	Ser	Gln
Tyr	Leu	Leu 115	Thr	Ala	Ile	His	Lys 120	Trp	Asp	Lys	Lys	Asn 125	Lys	Glu	Phe
Lys	Asn 130	Phe	Met	Lys	Lys	Met 135	Lys	Asn	His	Glu	Cys 140	Pro	Thr	Phe	Gln
Ser	Val	Phe	Lys												

000260"69594960


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<210> 115
<211> 45
<212> PRT
<213> homo sapiens
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Pro 1	Val	Ile	Tyr	Ser 5	Val	Leu	Ile	Arg	Ser 10	Glu	Ile	Arg	Tyr	Lys 15	Ile
Ser	Arg	Pro	Val 20	Thr	Thr	Asp	Phe	Ile 25	Lys	Ser	Glu	Ser	Leu 30	Ile	Leu
Ala	Cys	Leu 35	Tyr	Leu	Ile	Ser	Glu 40	Arg	Met	Ser	Thr	Leu 45			

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<210> 116
<211> 40
<212> PRT
<213> homo sapiens
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Pro 1	Asp	Cys	Glu	Ser 5	Phe	Met	Tyr	Phe	Asn 10	Leu	Asp	Ser	Val	Phe 15	Leu
Arg	Val	Leu	Ser 20	Met	Lys	Leu	Ala	Asp 25	Ser	Arg	Gln	Asp	Ser 30	Phe	Phe
His	His	Gly 35	Trp	Leu	Ile	Ser	Pro 40								

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<210> 117
<211> 27
<212> PRT
<213> homo sapiens
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Thr 1	Asn	Glu	His	Thr 5	Leu	Thr	Ser	Tyr	Leu 10	Gln	Leu	Pro	Phe	Ser 15	Phe
Asn	Arg	Ile	Val 20	Lys	Ala	Ser	Cys	Ile 25	Leu	Ile					

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<210> 118
<400> 118
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<210> 119
<211> 135
<212> PRT
<213> homo sapiens
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Arg 1	Ser	Asn	Ala	Val 5	Gln	Leu	Thr	Arg	Met 10	Glu	Tyr	Ala	Met	Lys 15	Ser
Leu	Ser	Leu	Leu	Tyr	Pro	Lys	Ser	Leu	Ser	Arg	His	Val	Ser	Val	Arg

000260" 69594960

				20				62		25				30		
Thr	Ser	Val	Val	Thr	Gln	Gln	Leu	Leu	Ser	Glu	Pro	Ser	Pro	Lys	Ala	
		35					40					45				
Pro	Arg	Ala	Arg	Pro	Cys	Arg	Val	Ser	Thr	Ala	Asp	Arg	Ser	Val	Arg	
	50					55					60					
Lys	Gly	Ile	Met	Ala	Tyr	Ser	Leu	Glu	Asp	Leu	Leu	Leu	Lys	Val	Arg	
65					70					75					80	
Asp	Thr	Leu	Met	Leu	Ala	Asp	Lys	Pro	Phe	Phe	Leu	Val	Leu	Glu	Glu	
				85					90					95		
Asp	Gly	Thr	Thr	Val	Glu	Thr	Glu	Glu	Tyr	Phe	Gln	Ala	Leu	Ala	Gly	
			100					105					110			
Asp	Thr	Val	Phe	Met	Val	Leu	Gln	Lys	Gly	Gln	Lys	Trp	Gln	Pro	Pro	
		115					120					125				
Ser	Glu	Gln	Gly	Thr	Arg	His										
	130					135										
<210>	120															
<400>	120															
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<210>	121															
<400>	121															
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<210>	122															
<211>	193															
<212>	PRT															
<213>	homo sapiens															
<400>	122															
Glu	Ala	Cys	Ala	His	Thr	Leu	Ser	Cys	Pro	Ala	Leu	Ala	Arg	Leu	Gly	
1				5					10					15		
Arg	Ala	Arg	Arg	Arg	Pro	Trp	Met	Ser	His	Arg	Thr	Ser	Ser	Thr	Phe	
			20					25					30			
Arg	Ala	Glu	Arg	Ser	Phe	His	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ala	Ala	
		35					40					45				
Thr	Ser	Ser	Ser	Ala	Ser	Arg	Ala	Leu	Pro	Ala	Gln	Asp	Pro	Pro	Met	
	50					55					60					
Glu	Lys	Ala	Leu	Ser	Met	Phe	Ser	Asp	Asp	Phe	Gly	Ser	Phe	Met	Arg	
65					70					75					80	
Pro	His	Ser	Glu	Pro	Leu	Ala	Phe	Pro	Ala	Arg	Pro	Gly	Gly	Ala	Gly	

000260"69594650

				85			63		90				95			
Asn	Ile	Lys	Thr	Leu	Gly	Asp	Ala	Tyr	Glu	Phe	Ala	Val	Asp	Val	Arg	
			100					105					110			
Asp	Phe	Ser	Pro	Glu	Asp	Ile	Ile	Val	Thr	Thr	Ser	Asn	Asn	His	Ile	
		115					120					125				
Glu	Val	Arg	Ala	Glu	Lys	Leu	Ala	Ala	Asp	Gly	Thr	Val	Met	Asn	Thr	
	130					135					140					
Phe	Ala	His	Lys	Cys	Gln	Leu	Pro	Glu	Asp	Val	Asp	Pro	Thr	Ser	Val	
145					150					155					160	
Thr	Ser	Ala	Leu	Arg	Glu	Asp	Gly	Ser	Leu	Thr	Ile	Arg	Ala	Arg	Arg	
				165					170					175		
His	Pro	His	Thr	Glu	His	Val	Gln	Gln	Thr	Phe	Arg	Thr	Glu	Ile	Lys	
			180					185					190			

Ile

<210> 123
<400> 123
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<210> 124
<211> 38
<212> PRT
<213> homo sapiens

<400> 124

Met	Ala	Thr	Phe	Tyr	Pro	Leu	Phe	Pro	Asn	Gly	Gly	Gly	Thr	Tyr	Pro	
1				5					10					15		
Glu	Val	Val	Asn	Asp	Phe	Pro	Leu	Lys	Leu	Leu	Tyr	Phe	Thr	Asn	Leu	
			20					25					30			

Asn	Tyr	Phe	Val	Leu	Met											
		35														

<210> 125
<211> 65
<212> PRT
<213> homo sapiens

<400> 125

Met	Trp	Leu	Phe	His	Asp	Ala	Gly	Ile	Arg	Ser	Ala	Gly	Gly	Leu	Ser	
1				5					10					15		
Leu	Leu	Ser	Cys	Gly	Ser	Trp	Pro	Leu	Pro	Ser	Gly	Tyr	His	Arg	Leu	
			20					25					30			

Gln	Asp	Thr	Asn	Gly	Gln	Gln	Lys	Asn	Val	Thr	Leu	Leu	Ile	Leu	Ser	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

35 64 45
 40
 Ser Ser Ser Ile Gly Thr Lys Leu Pro Ser Arg Pro Arg Glu Ile Leu
 50 55 60
 Cys
 65
 <210> 126
 <211> 250
 <212> PRT
 <213> homo sapiens
 <400> 126
 Glu Thr Arg Val Lys Thr Ser Leu Glu Leu Leu Arg Thr Gln Leu Glu
 1 5 10 15
 Pro Thr Gly Thr Val Gly Asn Thr Ile Met Thr Ser Gln Pro Val Pro
 20 25 30
 Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
 35 40 45
 Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
 50 55 60
 His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
 65 70 75 80
 Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
 85 90 95
 Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
 100 105 110
 Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile
 115 120 125
 Ala Thr Glu Lys Arg Leu Thr Lys Leu Leu Val His Ser Ser Leu Val
 130 135 140
 Gly Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Ile Leu
 145 150 155 160
 Ser Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Gln Cys Glu Leu
 165 170 175
 Asp Lys Asn Asn Ile Pro Thr Arg Ser Tyr Val Ser Tyr Phe Tyr His
 180 185 190
 Asp Ser Leu Tyr Thr Thr Asp Cys Tyr Thr Ala Lys Ala Ser Leu Ala

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							65								
		195					200					205			
Gly	Thr 210	Leu	Ser	Leu	Met	Leu 215	Ile	Cys	Thr	Leu	Leu 220	Glu	Phe	Cys	Leu
Ala 225	Val	Leu	Thr	Ala	Val 230	Leu	Arg	Trp	Lys	Gln 235	Ala	Tyr	Ser	Asp	Phe 240
Pro	Gly	Val	Ser	Val 245	Leu	Ala	Gly	Phe	Thr 250						
<210> 127															
<400> 127															
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<210> 128															
<211> 61															
<212> PRT															
<213> homo sapiens															
<400> 128															
Met 1	His	Thr	Cys	Gln 5	Ile	Tyr	Ile	Tyr	Ser 10	Thr	Asn	Val	Thr	Phe 15	Leu
Phe	Phe	Val	Leu 20	Asp	Val	Arg	Ala	Cys 25	Ser	Tyr	Val	Arg	Tyr 30	Leu	His
Lys	Leu	Leu 35	His	Tyr	Phe	Phe	Leu 40	Cys	Asn	Thr	Phe	Leu 45	Phe	Val	Tyr
Val	Val 50	Gln	Ile	Tyr	Ser	Phe 55	Leu	Lys	Leu	Leu	Lys 60	Lys			
<210> 129															
<211> 211															
<212> PRT															
<213> homo sapiens															
<400> 129															
Pro 1	Ala	Ser	Asn	Arg 5	Pro	Lys	Ser	Gly	Arg 10	Ala	Pro	Glu	Pro	Arg 15	Glu
Pro	Ala	Arg	Arg 20	Ser	Ala	Gly	Gly	Ser 25	Pro	Pro	Pro	Pro	Pro 30	Trp	Pro
Arg	Val	Pro 35	Ala	Ala	Ala	Ala	Gly 40	Thr	Glu	Gly	Ala	Ser 45	Pro	Asp	Leu
Ala	Pro 50	Leu	Arg	Pro	Ala	Ala 55	Pro	Gly	Gln	Thr	Pro 60	Leu	Arg	Lys	Glu
Val 65	Leu	Lys	Ser	Lys	Met 70	Gly	Lys	Ser	Glu	Lys 75	Ile	Ala	Leu	Pro	His 80

Gly	Gln	Leu	Val	His 85	Gly	Ile	His ⁶⁶	Leu	Tyr 90	Glu	Gln	Pro	Lys	Ile 95	Asn	
Arg	Gln	Lys	Ser 100	Lys	Tyr	Asn	Leu	Pro 105	Leu	Thr	Lys	Ile	Thr 110	Ser	Ala	
Lys	Arg	Asn 115	Glu	Asn	Asn	Phe	Trp 120	Gln	Asp	Ser	Val	Ser 125	Ser	Asp	Arg	
Ile	Gln 130	Lys	Gln	Glu	Lys	Lys 135	Pro	Phe	Lys	Asn	Thr 140	Glu	Asn	Ile	Lys	
Asn 145	Ser	His	Leu	Lys	Lys 150	Ser	Ala	Phe	Leu	Thr 155	Glu	Val	Ser	Gln	Lys 160	
Glu	Asn	Tyr	Ala	Gly 165	Ala	Lys	Phe	Ser	Asp 170	Pro	Pro	Ser	Pro	Ser 175	Val	
Leu	Pro	Lys	Pro 180	Pro	Ser	His	Trp	Met 185	Gly	Ser	Thr	Val	Glu 190	Asn	Ser	
Asn	Gln	Asn 195	Arg	Glu	Leu	Met	Ala 200	Val	His	Leu	Lys	Thr 205	Leu	Leu	Lys	
Val	Gln 210	Thr														

<210> 130
<400> 130
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<210> 131
<211> 48
<212> PRT
<213> homo sapiens

<400> 131

Met 1	Ile	Leu	Thr	Asn 5	Pro	Leu	Lys	Ser	Lys 10	Thr	Asp	Thr	Phe	Ile 15	Asn	
Arg	Ser	Ile	Cys 20	Lys	Gln	Ser	Gln	Tyr 25	Ala	Leu	Gly	Arg	Leu 30	Thr	Ile	
Phe	Leu	Thr 35	Cys	Gln	Gly	Val	Leu 40	Pro	Ser	Gln	Gln	Thr 45	Pro	Leu	Ile	

<210> 132
<211> 78
<212> PRT
<213> homo sapiens

<400> 132

Leu	Gly	Ile	Phe	Leu	His	Gln	Tyr	Val	Ile	Phe	Asn	Gln	Asn	Val	Lys	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

000260"69594960

1				5			67		10			15			
Phe	Leu	Leu	Asn 20	Ser	Leu	Pro	Ala	Ile 25	Val	Ile	Val	Pro	Ser 30	Trp	Pro
Thr	Trp	Phe 35	Pro	Asp	Val	Val	Asn 40	Asn	Ile	Asn	Ala	Ser 45	Ala	Val	Gly
Pro	Leu 50	Leu	Arg	Cys	Leu	Arg 55	Arg	Asn	Phe	Val	Leu 60	Ala	Ile	Ser	Ile
Asn 65	Phe	Val	Phe	Tyr	Leu 70	Gln	Phe	Gly	Arg	Arg 75	Lys	Val	Thr		

<210> 133
 <211> 72
 <212> PRT
 <213> homo sapiens

Met 1	Asp	Met	Ala	Lys 5	Thr	Lys	Phe	Leu	Arg 10	Arg	His	Leu	Ser	Lys 15	Gly
Pro	Thr	Ala	Asp 20	Ala	Leu	Met	Leu	Phe 25	Thr	Thr	Ser	Gly	Asn 30	Gln	Val
Gly	His	Asp 35	Gly	Thr	Ile	Thr	Met 40	Ala	Gly	Asn	Glu	Phe 45	Asn	Lys	Asn
Phe	Thr 50	Phe	Trp	Leu	Lys	Ile 55	Thr	Tyr	Trp	Cys	Lys 60	Lys	Ile	Pro	Asn
Gln 65	Ile	Lys	Ser	Tyr	Cys 70	Phe	Asp								

<210> 134
 <400> 134
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 <210> 135
 <211> 87
 <212> PRT
 <213> homo sapiens

Leu 1	Asn	Val	Phe	Ser 5	Ser	Leu	Gln	Ile	Ser 10	Glu	Leu	Ile	Phe	Pro 15	Pro
Leu	Pro	Met	Trp 20	His	Pro	Leu	Pro	Arg 25	Lys	Lys	Pro	Gly	Met 30	Tyr	Arg
Gly	Asn	Gly 35	His	Gln	Asn	His	Tyr 40	Pro	Pro	Pro	Val	Pro 45	Phe	Gly	Tyr
Pro	Asn	Gln	Gly	Arg	Lys	Asn	Lys	Pro	Tyr	Arg	Pro	Ile	Pro	Val	Thr

000260" 69594960

09545559 092000

65				70				69				75				80			
Asp	Phe	Pro	Ala	Glu 85	Gln	Val	Asp	Asp	Leu 90	Asn	Leu	Thr	Ser	Gly 95	Glu				
Ile	Val	Tyr	Leu 100	Leu	Glu	Lys	Ile	Asp 105	Thr	Asp	Trp	Tyr	Arg 110	Gly	Asn				
Cys	Arg	Asn 115	Gln	Ile	Gly	Ile	Phe 120	Pro	Ala	Asn	Tyr	Val 125	Lys	Val	Ile				
Ile	Asp 130	Ile	Pro	Glu	Gly	Gly 135	Asn	Gly	Lys	Arg	Glu 140	Cys	Val	Ser	Ser				
His 145	Cys	Val	Lys	Gly	Ser 150	Arg	Cys	Val	Ala	Arg 155	Phe	Glu	Tyr	Ile	Gly 160				
Glu	Gln	Lys	Asp	Glu 165	Leu	Ser	Phe	Ser	Glu 170	Gly	Glu	Ile	Ile	Ile 175	Leu				
Lys	Glu	Tyr	Val 180	Asn	Glu	Glu	Trp	Ala 185	Arg	Gly	Glu	Val	Arg 190	Gly	Arg				
Thr	Gly	Ile 195	Phe	Pro	Leu	Asn	Phe 200	Val	Glu	Pro	Val	Glu 205	Asp	Tyr	Pro				
Thr	Ser 210	Gly	Ala	Asn	Val	Leu 215	Ser	Thr	Lys	Val	Pro 220	Leu	Lys	Thr	Lys				
Lys 225	Glu	Asp	Ser	Gly	Ser 230	Asn	Ser	Gln	Val	Asn 235	Ser	Leu	Pro	Ala	Glu 240				
Trp	Cys	Glu	Ala	Leu 245	His	Ser	Phe	Thr	Ala 250	Glu	Thr	Ser	Asp	Asp 255	Leu				
Ser	Phe	Lys	Arg 260	Gly	Asp	Arg	Ile	Gln 265	Ile	Leu	Glu	Arg	Leu 270	Asp	Ser				
Asp	Trp	Cys 275	Arg	Gly	Arg	Leu	Gln 280	Asp	Arg	Glu	Gly	Ile 285	Phe	Pro	Ala				
Val	Phe 290	Val	Arg	Pro	Cys	Pro 295	Ala	Glu	Ala	Lys	Ser 300	Met	Leu	Ala	Ile				
Val 305	Pro	Lys	Gly	Arg	Lys 310	Ala	Lys	Ala	Leu	Tyr 315	Asp	Phe	Arg	Gly	Glu 320				
Asn	Glu	Asp	Glu	Leu 325	Ser	Phe	Lys	Ala	Gly 330	Asp	Ile	Ile	Thr	Glu 335	Leu				

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<210> 142
<211> 46
<212> PRT
<213> homo sapiens
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<400> 142

Met	Pro	Phe	Leu	Arg	Lys	Phe	Asp	Arg	Leu	Val	Arg	Thr	Ser	Asp	His
1				5					10					15	
Gln	Ile	Ser	Leu	Lys	Trp	Val	Ser	Trp	Asn	Phe	Ile	Phe	Asp	Asn	Ile
			20					25					30		
Tyr	Thr	Ile	Pro	Asn	Ser	Phe	Ala	Val	Leu	Arg	Phe	Val	Gly		
		35					40					45			

<210> 143

<211> 56

<212> PRT

<213> homo sapiens

<400> 143

Met	Glu	Gly	Trp	Gly	Met	Ser	Ser	Ile	Asn	Pro	Tyr	Gly	Met	His	Ser
1				5					10					15	
Gln	Trp	Pro	Ser	His	Leu	Gly	Leu	Glu	Pro	Leu	Val	Gln	Gly	Leu	Gly
			20					25					30		
Glu	Asn	Arg	Pro	His	Gly	Asn	Ser	His	Thr	Val	Ile	Ala	Phe	Asn	Thr
		35					40					45			
Glu	Pro	Arg	Val	Pro	Lys	Gln	Gln								
	50					55									

<210> 144

<211> 56

<212> PRT

<213> homo sapiens

<400> 144

Met	Asn	Ile	Ser	Thr	Gln	Gly	Arg	Ala	Lys	Gly	Val	Pro	Arg	Ile	Leu
1				5					10					15	
Leu	Ala	Lys	Gly	Gln	Val	Leu	Ile	Glu	Gly	Leu	Glu	Leu	Ser	Arg	Phe
			20					25					30		
Met	Glu	Ala	Ala	Cys	Thr	Leu	Gly	Ala	Cys	Pro	Asp	Ser	Ser	Leu	Gly
		35					40					45			
Phe	Pro	Phe	Tyr	Leu	Ser	Ser	Phe								
	50					55									

<210> 145

<211> 109

<212> PRT

<213> homo sapiens

<400> 145

Met	Pro	Lys	Gly	Lys	Ala	Phe	Arg	Arg	Thr	Leu	Arg	Ile	Thr	Ser	Leu
1				5					10					15	

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Phe	Phe	Ser	Ser 20	Leu	Leu	Leu	Leu ⁷²	Gln 25	Leu	Leu	Phe	Gly	His 30	His	Leu
Leu	Val	Leu 35	Val	Ser	Pro	Gln	Leu 40	Pro	Gly	Ala	Val	Phe 45	Glu	Gly	Glu
Ala	Phe 50	Ser	Val	Pro	Pro	Pro 55	Gln	Ala	Leu	Pro	Met 60	Met	Ala	Pro	Ser
His 65	His	Pro	Ser	Pro	Ala 70	Pro	Leu	Pro	Ala	Ser 75	Pro	Pro	Pro	Pro	Ala 80
Pro	Pro	Pro	Pro	Trp 85	Arg	Arg	Arg	Gly	Ile 90	Pro	Leu	Ala	Phe	Gly 95	Leu
Pro	Arg	Ser	Arg 100	Arg	Leu	Pro	Glu	Leu 105	Pro	Gln	Pro	Arg			

<210> 146
 <211> 247
 <212> PRT
 <213> homo sapiens
 <400> 146

Arg 1	Pro	Ala	Pro	Ala 5	Pro	Arg	Cys	Gln	Leu 10	Pro	Gln	Arg	Pro	Ala 15	Glu
Ala	Arg	Cys	Met 20	Leu	Ser	Arg	Cys	Arg 25	Ser	Arg	Leu	Leu	His 30	Val	Leu
Gly	Leu	Ser 35	Phe	Leu	Leu	Gln	Thr 40	Arg	Arg	Pro	Ile	Leu 45	Leu	Cys	Ser
Pro	Arg 50	Leu	Met	Lys	Pro	Leu 55	Val	Val	Phe	Val	Leu 60	Gly	Gly	Pro	Gly
Ala 65	Gly	Lys	Gly	Thr	Gln 70	Cys	Ala	Arg	Ile	Val 75	Glu	Lys	Tyr	Gly	Tyr 80
Thr	His	Leu	Ser	Ala 85	Gly	Glu	Leu	Leu	Arg 90	Asp	Glu	Arg	Lys	Asn 95	Pro
Asp	Ser	Gln	Tyr 100	Gly	Glu	Leu	Ile	Glu 105	Lys	Tyr	Ile	Lys	Glu 110	Gly	Lys
Ile	Val	Pro 115	Val	Glu	Ile	Thr	Ile 120	Ser	Leu	Leu	Lys	Arg 125	Glu	Met	Asp
Gln	Thr 130	Met	Ala	Ala	Asn	Ala 135	Gln	Lys	Asn	Lys	Phe 140	Leu	Ile	Asp	Gly

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Asp Ala Leu Val Gln Lys His ⁷⁴Leu Thr Lys Leu Arg His Trp Gln Gln
 130 135 140
 Val Leu Glu Asp Ile Asn Val Gln His Lys Lys Pro Ala Asp Ile Pro
 145 150 155 160
 Gln Gly Ser Leu Ala Tyr Leu Glu Gln Ala Ser Ala Asn Ile Pro Ala
 165 170 175
 Pro Leu Lys Pro Thr
 180

<210> 148
 <211> 236
 <212> PRT
 <213> homo sapiens

<400> 148

Met Leu Arg Asp Leu Gln Leu Gln Ile Leu Arg Asn Val Thr His His
 1 5 10 15
 Val Ser Val Thr Lys Gln Leu Pro Thr Ser Glu Ala Val Val Ser Ala
 20 25 30
 Val Ser Glu Ala Gly Ala Ser Gly Ile Thr Glu Ala Gln Ala Arg Ala
 35 40 45
 Ile Val Asn Ser Ala Leu Lys Leu Tyr Ser Gln Asp Lys Thr Gly Met
 50 55 60
 Val Asp Phe Ala Leu Glu Ser Gly Gly Gly Ser Ile Leu Ser Thr Arg
 65 70 75 80
 Cys Ser Glu Thr Tyr Glu Thr Lys Thr Ala Leu Met Ser Leu Phe Gly
 85 90 95
 Ile Pro Leu Trp Tyr Phe Ser Gln Ser Pro Arg Val Val Ile Gln Pro
 100 105 110
 Asp Ile Tyr Pro Gly Asn Cys Trp Ala Phe Lys Gly Ser Gln Gly Tyr
 115 120 125
 Leu Val Val Arg Leu Ser Met Met Ile His Pro Ala Ala Phe Thr Leu
 130 135 140
 Glu His Ile Pro Lys Thr Leu Ser Pro Thr Gly Asn Ile Ser Ser Ala
 145 150 155 160
 Pro Lys Asp Phe Ala Val Tyr Gly Leu Glu Asn Glu Tyr Gln Glu Glu
 165 170 175

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Gly	Gln	Leu	Leu	Gly	Gln	Phe	Thr	Tyr	Asp	Gln	Asp	Gly	Glu	Ser	Leu
			180					185					190		
Gln	Met	Phe	Gln	Ala	Leu	Lys	Arg	Pro	Asp	Asp	Thr	Ala	Phe	Gln	Ile
		195					200					205			
Val	Glu	Leu	Arg	Ile	Phe	Ser	Asn	Trp	Gly	His	Pro	Glu	Tyr	Thr	Cys
	210					215					220				
Leu	Tyr	Arg	Phe	Arg	Val	His	Gly	Glu	Pro	Val	Lys				
225					230					235					

<210> 149
 <211> 57
 <212> PRT
 <213> homo sapiens

Met	Glu	Trp	Ser	Pro	Ser	Ala	Ser	Leu	Phe	Asn	Pro	His	Ile	Trp	Ser
1				5					10					15	
Thr	Arg	Val	Asp	Leu	Trp	Leu	Thr	Thr	Tyr	Thr	Met	Leu	Lys	Ser	Ser
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			20					25					30		
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305 310 315 320

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325 330 335

Leu Glu Leu Arg Glu Gly Asp Arg Val Asp Val Met Gln Gln Cys Asp
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2411

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3265

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<211> 262

<212> PRT

<213> homo sapiens

<400> 179

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Gly	Met	Pro 35	Ala	Pro	Leu	Gly	Tyr 40	Val	Pro	Gly	Leu	Gly 45	Arg	Gly	Ala
Thr	Gly 50	Phe	Thr	Thr	Arg	Ser 55	Asp	Ile	Gly	Pro	Ala 60	Arg	Asp	Ala	Asn
Asp 65	Pro	Val	Asp	Asp	Arg 70	His	Ala	Pro	Pro	Gly 75	Lys	Arg	Thr	Val	Gly 80
Asp	Gln	Met	Lys	Lys 85	Asn	Gln	Ala	Ala	Asp 90	Asp	Asp	Asp	Glu	Asp 95	Leu
Asn	Asp	Thr	Asn 100	Tyr	Asp	Glu	Phe	Asn 105	Gly	Tyr	Ala	Gly	Ser 110	Leu	Phe
Ser	Ser	Gly 115	Pro	Tyr	Glu	Lys	Asp 120	Asp	Glu	Glu	Ala	Asp 125	Ala	Ile	Tyr
Ala	Ala 130	Leu	Asp	Lys	Arg	Met 135	Asp	Glu	Arg	Arg	Lys 140	Glu	Arg	Arg	Glu

000260" 69594660

Gln 145	Arg	Glu	Lys	Glu	Glu 150	Ile	Glu	Lys	Tyr	Arg 155	Met	Glu	Arg	Pro	Lys 160
Ile	Gln	Gln	Gln	Phe 165	Ser	Asp	Leu	Lys	Arg 170	Lys	Leu	Ala	Glu	Val 175	Thr
Glu	Glu	Glu	Trp 180	Leu	Ser	Ile	Pro	Glu 185	Val	Gly	Asp	Ala	Arg 190	Asn	Lys
Arg	Gln	Arg 195	Asn	Pro	Arg	Tyr	Glu 200	Lys	Leu	Thr	Pro	Val 205	Pro	Asp	Ser
Phe	Phe 210	Ala	Lys	His	Leu	Gln 215	Thr	Gly	Glu	Asn	His 220	Thr	Ser	Val	Asp
Pro 225	Arg	Gln	Thr	Gln	Phe 230	Gly	Gly	Leu	Asn	Thr 235	Pro	Tyr	Pro	Gly	Gly 240
Leu	Asn	Thr	Pro	Tyr 245	Pro	Gly	Gly	Met	Thr 250	Pro	Gly	Leu	Met	Thr 255	Pro
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Ala	Arg	Thr	Asp 20	Asp	Thr	Trp	His	Ser 25	Glu	Leu	Asp	Met	Arg 30	Lys	Ile
Gly	Gln	Ala 35	Arg	Asn	Thr	Leu	Met 40	Asp	Met	Arg	Leu	Ser 45	Gln	Val	Ser
Asp	Ser 50	Val	Ser	Gly	Gln	Thr 55	Val	Val	Asp	Pro	Lys 60	Gly	Tyr	Leu	Thr
Asp 65	Leu	Asn	Ser	Met	Ile 70	Pro	Thr	His	Gly	Gly 75	Asp	Ile	Asn	Asp	Ile 80
Lys	Lys	Ala	Arg	Leu 85	Leu	Leu	Lys	Ser	Val 90	Arg	Glu	Thr	Asn	Pro 95	His
His	Pro	Pro	Ala 100	Trp	Ile	Ala	Ser	Ala 105	Arg	Leu	Glu	Glu	Val 110	Thr	Gly

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Lys	Leu	Gln 115	Val	Ala	Arg	Asn	Leu 120	Ile	Met	Lys	Gly	Thr 125	Glu	Met	Cys
Pro	Lys 130	Ser	Glu	Asp	Val	Trp 135	Leu	Glu	Ala	Ala	Arg 140	Leu	Gln	Pro	Gly
Asp 145	Thr	Ala	Lys	Ala	Val 150	Val	Ala	Gln	Ala	Val 155	Arg	His	Leu	Pro	Gln 160
Ser	Val	Arg	Ile	Tyr 165	Ile	Arg	Ala	Ala	Glu 170	Leu	Glu	Thr	Asp	Ile 175	Arg
Ala	Lys	Lys	Arg 180	Val	Leu	Arg	Lys	Ala 185	Leu	Glu	His	Val	Pro 190	Asn	Ser
Val	Arg	Leu 195	Trp	Lys	Ala	Ala	Val 200	Glu	Leu	Glu	Glu	Pro 205	Glu	Asp	Ala
Arg	Ile 210	Met	Leu	Ser	Arg	Ala 215	Val	Glu	Cys	Cys	Pro 220	Thr	Ser	Val	Glu
Leu 225	Trp	Leu	Ala	Leu	Ala 230	Arg	Leu	Glu	Thr	Tyr 235	Glu	Asn	Ala	Arg	Lys 240
Val	Leu	Asn	Lys	Ala 245	Arg	Glu	Asn	Ile	Pro 250	Thr	Asp	Arg	His	Ile 255	Trp
Ile	Thr	Ala	Ala 260	Lys	Leu	Glu	Glu	Ala 265	Asn	Gly	Asn	Thr	Gln 270	Met	Val
Glu	Lys	Ile 275	Ile	Asp	Arg	Ala	Ile 280	Thr	Ser	Leu	Arg	Ala 285	Asn	Gly	Val
Glu	Ile 290	Asn	Arg	Glu	Gln	Trp 295	Ile	Gln	Asp	Ala	Glu 300	Glu	Cys	Asp	Arg
Ala 305	Gly	Ser	Val	Ala	Thr 310	Cys	Gln	Ala	Val	Met 315	Arg	Ala	Val	Ile	Gly 320
Ile	Gly	Ile	Glu	Glu 325	Glu	Asp	Arg	Lys	His 330	Thr	Trp	Met	Glu	Asp 335	Ala
Asp	Ser	Cys	Val 340	Ala	His	Asn	Ala	Leu 345	Glu	Cys	Ala	Arg	Ala 350	Ile	Tyr
Ala	Tyr	Ala 355	Leu	Gln	Val	Phe	Pro 360	Ser	Lys	Lys	Ser	Val 365	Trp	Leu	Arg

000260" 6954860



Ala	Ala	Tyr	Phe	Glu	Lys	Asn	His	Gly	Thr	Arg	Glu	Ser	Leu	Glu	Ala
	370					375					380				

Leu	Leu	Gln	Arg	Ala	Val	Ala	His	Cys	Pro	Lys	Ala	Glu	Val	Leu	Trp
385					390					395					400

Leu	Met	Gly	Ala	Lys	Ser	Lys	Trp	Leu	Ala	Gly	Asp	Val	Pro	Ala	Ala
				405					410					415	

Arg	Ser	Ile	Leu	Ala	Leu	Ala	Phe	Gln	Ala	Asn	Pro	Asn	Ser	Glu	Glu
			420					425					430		

Ile	Trp	Leu	Ala	Ala	Val	Lys	Leu	Glu	Ser	Glu	Asn	Asp	Glu	Tyr	Glu
		435					440					445			

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Gly	Cys	Ser
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<210> 181

<211> 284

<212> PRT

<213> homo sapiens

<400> 181

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Thr	Ala	Arg	Val	Phe	Met	Lys	Ser	Val	Lys	Leu	Glu	Trp	Val	Gln	Asp
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Asn	Ile	Arg	Ala	Ala	Gln	Asp	Leu	Cys	Glu	Glu	Ala	Leu	Arg	His	Tyr
		35					40					45			

Glu	Asp	Phe	Pro	Lys	Leu	Trp	Met	Met	Lys	Gly	Gln	Ile	Glu	Glu	Gln
	50					55					60				

Lys	Glu	Met	Met	Glu	Lys	Ala	Arg	Glu	Ala	Tyr	Asn	Gln	Gly	Leu	Lys
65					70					75					80

Lys	Cys	Pro	His	Ser	Thr	Pro	Leu	Trp	Leu	Leu	Leu	Ser	Arg	Leu	Glu
				85					90					95	

Glu	Lys	Ile	Gly	Gln	Leu	Thr	Arg	Ala	Arg	Ala	Ile	Leu	Glu	Lys	Ser
			100					105					110		

Arg	Leu	Lys	Asn	Pro	Lys	Asn	Pro	Gly	Leu	Trp	Leu	Glu	Ser	Val	Arg
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<210> 183
 <211> 75
 <212> PRT
 <213> homo sapiens

<400> 183

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Glu	Phe	Gln	Arg 20	Arg	Leu	Leu	Leu	Lys 25	Cys	Leu	Leu	Ala	Ala 30	Gln	Tyr
Gln	Ser	Ile 35	Asn	Tyr	Pro	Phe	Trp 40	Gly	Leu	Ala	Leu	Glu 45	Ile	Ile	Phe
Val	Gly 50	Arg	Pro	Asn	Ser	Ser 55	Gln	Gln	Gly	Ser	Gln 60	Ala	Cys	Leu	Leu
Asp 65	Leu	Phe	Pro	Leu	Arg 70	Gly	Arg	Asn	Glu	Leu 75					

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 <211> 117
 <212> PRT
 <213> homo sapiens

<400> 184

Gln 1	Gly	Thr	Arg	His 5	Pro	Gln	Ser	Leu	Ser 10	His	Lys	Pro	Ala	Lys 15	Lys
Ile	Asp	Val	Ala 20	Arg	Val	Thr	Phe	Asp 25	Leu	Tyr	Lys	Leu	Asn 30	Pro	Gln
Asp	Phe	Ile 35	Gly	Cys	Leu	Asn	Val 40	Lys	Ala	Thr	Phe	Tyr 45	Asp	Thr	Tyr
Ser	Leu 50	Ser	Tyr	Asp	Leu	His 55	Cys	Cys	Gly	Ala	Lys 60	Arg	Ile	Met	Lys
Glu 65	Ala	Phe	Arg	Trp	Ala 70	Leu	Phe	Ser	Met	Gln 75	Ala	Thr	Gly	His	Val 80
Leu	Leu	Gly	Thr	Ser 85	Cys	Tyr	Leu	Gln	Gln 90	Leu	Leu	Asp	Ala	Thr 95	Glu
Glu	Gly	Gln	Pro 100	Pro	Lys	Gly	Lys	Ala 105	Ser	Ser	Leu	Ile	Pro 110	Thr	Cys
Leu	Lys	Ile 115	Leu	Gln											

<210> 185
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 <212> PRT

000260" 69594960

100

<213> homo sapiens

<400> 185

Lys 1	Ser	Ala	Ala	Gln 5	Thr	Ala	Met	Thr	Thr 10	Pro	Pro	Gln	Thr	Pro 15	Pro
His	Pro	Tyr	Phe 20	Ile	Asn	Arg	Gln	Asp 25	Phe	Pro	Cys	Ile	Leu 30	Leu	Arg
Ile	Ser	Ser 35	Ser	His	Ser	Pro	Ala 40	Pro	Ser	Pro	Met	Ser 45	Trp	Leu	His
His	Cys 50	Lys	Thr	Asp	Leu	Leu 55	Gln	Gly	Ser	Gln	Lys 60	Leu	Leu	Leu	Ala
Leu 65	Tyr	His	Phe	Tyr	Pro 70	His	Leu	Pro	Pro	Glu 75	Thr	Ala	Thr	Ile	His 80
Ser	His	Cys	Pro	Ser 85	Ala	Leu	Arg	Pro	Ser 90	Ser	Arg	Ala	Asp	Gly 95	Ser
Met	Val	Ile	Leu 100	Ser	Trp	Val	Val	Leu 105	Leu	Lys	Pro	Ser	Gln 110	Gly	Ala
Asp	Ser	Gln 115	Arg	Ala	Ser	Arg	Val 120	Ser	Gly	Leu	Asp	Asp 125	Ser	Lys	Glu
Gly	Thr 130	Pro	Ile	Phe	Ile	Phe 135	Lys	Thr	Asp	Ile	Pro 140	Arg	Gly	Phe	

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<211> 84

<212> PRT

<213> homo sapiens

<400> 186

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Gly	Asn	Thr	Asp 20	Leu	Asp	Ile	His	Lys 25	Lys	Ile	Lys	Pro	Lys 30	Ile	Lys
His	Ser	Ile 35	Leu	Cys	Pro	Leu	Lys 40	Gly	Leu	Ile	Lys	Gly 45	Thr	Gln	Ser
Pro	Pro 50	Arg	Ser	Pro	Leu	Pro 55	Cys	Gln	His	His	Lys 60	Ala	Ser	Ser	Ala
His 65	Thr	Lys	Gly	Leu	Gly 70	Arg	Gly	Ile	Leu	Leu 75	Pro	Pro	His	Gln	Pro 80
Gln	Glu	Trp	Thr												

000260"092000

<400> 187

Thr Gln

<400> 188

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Ser	Leu	Leu	Val 20	Glu	Val	Ile	Asn	Arg 25	Phe	Lys	Glu	Lys	Ile 30	Leu	Ala
Val	Asn	Pro 35	Gln	Cys	Leu	Gln	Leu 40	Phe	Trp	Gln	Asn	Ile 45	Phe	Lys	Glu
Ile	Gln 50	Gln	Ala	Asn	Phe	Glu 55	Val	Leu	Met	Lys	Val 60	Lys	Glu	Gly	Gly
Ile 65	Ser	Ser	Phe	Gly	Arg 70	Asn	Glu	Lys	Cys	Leu 75	Thr	Arg	Asp	Ile	Thr 80
Thr	His	Val	Gly	Ser 85	Gly	Cys	Phe	Leu	Pro 90	Lys	Thr	Phe	Arg	Glu 95	Glu

Val Asn

<210> 189

<211> 437

<212> PRT

<213> homo sapiens

<400> 189

Lys 1	Tyr	Glu	Leu	Tyr 5	Thr	Glu	Asn	Ala	Thr 10	Thr	Glu	Lys	Thr	Glu 15	Pro
Asn	Ser	Gln	Glu 20	Asp	Lys	Asn	Asp	Gly 25	Gly	Lys	Ser	Arg	Lys 30	Gly	Asn
Ile	Glu	Leu 35	Ala	Ser	Ser	Glu	Pro 40	Gln	His	Phe	Thr	Thr 45	Thr	Val	Thr
Arg	Cys 50	Ser	Pro	Thr	Val	Ala 55	Phe	Val	Glu	Phe	Pro 60	Ser	Ser	Pro	Gln
Leu 65	Lys	Asn	Asp	Val	Ser 70	Glu	Glu	Lys	Asp	Gln 75	Lys	Lys	Pro	Glu	Asn 80
Glu	Met	Ser	Gly	Lys 85	Val	Glu	Leu	Val	Leu 90	Ser	Gln	Lys	Val	Val 95	Lys
Pro	Lys	Ser	Pro 100	Glu	Pro	Glu	Ala	Thr 105	Leu	Thr	Phe	Pro	Phe 110	Leu	Asp
Lys	Met	Pro 115	Glu	Ala	Asn	Gln	Leu 120	His	Leu	Pro	Asn	Leu 125	Asn	Ser	Gln
Val	Asp 130	Ser	Pro	Ser	Ser	Glu 135	Lys	Ser	Pro	Val	Met 140	Thr	Pro	Phe	Lys
Phe 145	Trp	Ala	Trp	Asp	Pro 150	Glu	Glu	Glu	Arg	Arg 155	Arg	Gln	Glu	Lys	Trp 160
Gln	Gln	Glu	Gln	Glu 165	Arg	Leu	Leu	Gln	Glu 170	Arg	Tyr	Gln	Lys	Glu 175	Gln
Asp	Lys	Leu	Lys 180	Glu	Glu	Trp	Glu	Lys 185	Ala	Gln	Lys	Glu	Val 190	Glu	Glu
Glu	Glu	Arg 195	Arg	Tyr	Tyr	Glu	Glu 200	Glu	Arg	Lys	Ile	Ile 205	Glu	Asp	Thr
Val	Val 210	Pro	Phe	Thr	Val	Ser 215	Ser	Ser	Ser	Ala	Asp 220	Gln	Leu	Ser	Thr

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Ser 225	Ser	Ser	Met	Thr	Glu 230	Gly	Ser	Gly	Thr	Met 235	Asn	Lys	Ile	Asp	Leu 240
Gly	Asn	Cys	Gln	Asp 245	Glu	Lys	Gln	Asp	Arg 250	Arg	Trp	Lys	Lys	Ser 255	Phe
Gln	Gly	Asp	Asp 260	Ser	Asp	Leu	Leu	Leu 265	Lys	Thr	Arg	Glu	Ser 270	Asp	Arg
Leu	Glu	Glu 275	Lys	Gly	Ser	Leu	Thr 280	Glu	Gly	Ala	Leu	Ala 285	His	Ser	Gly
Asn	Pro 290	Val	Ser	Lys	Gly	Val 295	His	Glu	Asp	His	Gln 300	Leu	Asp	Thr	Glu
Ala 305	Gly	Ala	Pro	His	Cys 310	Gly	Thr	Asn	Pro	Gln 315	Leu	Ala	Gln	Asp	Pro 320
Ser	Gln	Asn	Gln	Gln 325	Thr	Ser	Asn	Pro	Thr 330	His	Ser	Ser	Glu	Asp 335	Val
Lys	Pro	Lys	Thr 340	Leu	Pro	Leu	Asp	Lys 345	Ser	Ile	Asn	His	Gln 350	Ile	Glu
Ser	Pro	Ser 355	Glu	Arg	Arg	Lys	Ser 360	Ile	Ser	Gly	Lys	Lys 365	Leu	Cys	Ser
Ser	Cys 370	Gly	Leu	Pro	Leu	Gly 375	Lys	Gly	Ala	Ala	Met 380	Ile	Ile	Glu	Thr
Leu 385	Asn	Leu	Tyr	Phe	His 390	Ile	Gln	Cys	Phe	Arg 395	Cys	Gly	Ile	Cys	Lys 400
Gly	Gln	Leu	Gly	Asp 405	Ala	Val	Ser	Gly	Thr 410	Asp	Val	Arg	Ile	Arg 415	Asn
Gly	Leu	Leu	Asn 420	Cys	Asn	Asp	Cys	Tyr 425	Met	Arg	Ser	Arg	Ser 430	Ala	Gly
Gln	Pro	Thr 435	Thr	Leu											

<210> 190

<211> 331

<212> PRT

<213> homo sapiens

<400> 190

Ser 1	Ala	Asn	His	Lys 5	Leu	Glu	Val	Asn	Gly 10	Thr	Asp	Gly	Leu	Ala 15	Pro
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000260"69594960

Val	Glu	Val	Glu 20	Glu	Leu	Leu	Arg	Gln 25	Ala	Ser	Glu	Arg	Asn 30	Ser	Lys
Ser	Pro	Thr 35	Glu	Tyr	His	Glu	Pro 40	Val	Tyr	Ala	Asn	Pro 45	Phe	Tyr	Arg
Pro	Thr 50	Thr	Pro	Gln	Arg	Glu 55	Thr	Val	Thr	Pro	Gly 60	Pro	Asn	Phe	Gln
Glu 65	Arg	Ile	Lys	Ile	Lys 70	Thr	Asn	Gly	Leu	Gly 75	Ile	Gly	Val	Asn	Glu 80
Ser	Ile	His	Asn	Met 85	Gly	Asn	Gly	Leu	Ser 90	Glu	Glu	Arg	Gly	Asn 95	Asn
Phe	Asn	His	Ile 100	Ser	Pro	Ile	Pro	Pro 105	Val	Pro	His	Pro	Arg 110	Ser	Val
Ile	Gln	Gln 115	Ala	Glu	Glu	Lys	Leu 120	His	Thr	Pro	Gln	Lys 125	Arg	Leu	Met
Thr	Pro 130	Trp	Glu	Glu	Ser	Asn 135	Val	Met	Gln	Asp	Lys 140	Asp	Ala	Pro	Ser
Pro 145	Lys	Pro	Arg	Leu	Ser 150	Pro	Arg	Glu	Thr	Ile 155	Phe	Gly	Lys	Ser	Glu 160
His	Gln	Asn	Ser	Ser 165	Pro	Thr	Cys	Gln	Glu 170	Asp	Glu	Glu	Asp	Val 175	Arg
Tyr	Asn	Ile	Val 180	His	Ser	Leu	Pro	Pro 185	Asp	Ile	Asn	Asp	Thr 190	Glu	Pro
Val	Thr	Met 195	Ile	Phe	Met	Gly	Tyr 200	Gln	Gln	Ala	Glu	Asp 205	Ser	Glu	Glu
Asp	Lys 210	Lys	Phe	Leu	Thr	Gly 215	Tyr	Asp	Gly	Ile	Ile 220	His	Ala	Glu	Leu
Val 225	Val	Ile	Asp	Asp	Glu 230	Glu	Glu	Glu	Asp	Glu 235	Gly	Glu	Ala	Glu	Lys 240
Pro	Ser	Tyr	His	Pro 245	Ile	Ala	Pro	His	Ser 250	Gln	Val	Tyr	Gln	Pro 255	Ala
Lys	Pro	Thr	Pro 260	Leu	Pro	Arg	Lys	Arg 265	Ser	Glu	Ala	Ser	Pro 270	His	Glu

000260"69594950

Asn	Thr	Asn	His	Lys	Ser	Pro	His	Lys	Asn	Ser	Ile	Ser	Leu	Lys	Glu
		275					105 280					285			
Gln	Glu	Glu	Ser	Leu	Gly	Ser	Pro	Val	His	His	Ser	Pro	Phe	Asp	Ala
	290					295					300				
Gln	Thr	Thr	Gly	Asp	Gly	Thr	Glu	Asp	Pro	Ser	Leu	Thr	Ala	Leu	Arg
305					310					315					320
Met	Arg	Met	Ala	Lys	Leu	Gly	Lys	Lys	Val	Ile					
				325					330						

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 <211> 216
 <212> PRT
 <213> homo sapiens

<400> 191

Leu	Ser	Leu	Thr	Ser	Arg	Met	Glu	Glu	Ala	Glu	Leu	Val	Lys	Gly	Arg
1				5					10					15	
Leu	Gln	Ala	Ile	Thr	Asp	Lys	Arg	Lys	Ile	Gln	Glu	Glu	Ile	Ser	Gln
			20					25					30		
Lys	Arg	Leu	Lys	Ile	Glu	Glu	Asp	Lys	Leu	Lys	His	Gln	His	Leu	Lys
		35					40					45			
Lys	Lys	Ala	Leu	Arg	Glu	Lys	Trp	Leu	Leu	Asp	Gly	Ile	Ser	Ser	Gly
	50					55					60				
Lys	Glu	Gln	Glu	Glu	Met	Lys	Lys	Gln	Asn	Gln	Gln	Asp	Gln	His	Gln
65					70					75					80
Ile	Gln	Val	Leu	Glu	Gln	Ser	Ile	Leu	Arg	Leu	Glu	Lys	Glu	Ile	Gln
				85					90					95	
Asp	Leu	Glu	Lys	Ala	Glu	Leu	Gln	Ile	Ser	Thr	Lys	Glu	Glu	Ala	Ile
			100					105					110		
Leu	Lys	Lys	Leu	Lys	Ser	Ile	Glu	Arg	Thr	Thr	Glu	Asp	Ile	Ile	Arg
		115					120					125			
Ser	Val	Lys	Val	Glu	Arg	Glu	Glu	Arg	Ala	Glu	Glu	Ser	Ile	Glu	Asp
	130					135					140				
Ile	Tyr	Ala	Asn	Ile	Pro	Asp	Leu	Pro	Lys	Ser	Tyr	Ile	Pro	Ser	Arg
145					150					155					160
Leu	Arg	Lys	Glu	Ile	Asn	Glu	Glu	Lys	Glu	Asp	Asp	Glu	Gln	Asn	Arg
				165					170					175	

000260"69594960

Lys	Ala	Leu	Tyr 180	Ala	Met	Glu	Ile ¹⁰⁶ 185	Lys	Val	Glu	Lys	Asp	Leu 190	Lys	Thr
Gly	Glu	Ser 195	Thr	Val	Leu	Ser	Ser 200	Asn	Thr	Ser	Gly	His 205	Gln	Met	Thr
Leu	Lys 210	Gly	Thr	Gly	Val	Lys 215	Val								

<210> 192
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 <212> PRT
 <213> homo sapiens

<400> 192

Arg 1	Gly	Ala	Gly	Thr 5	Gln	Pro	Gly	Pro	Leu 10	Leu	Lys	Lys	Pro	Tyr 15	Gln
Pro	Arg	Ile	Lys 20	Ile	Ser	Lys	Thr	Ser 25	Val	Asp	Gly	Asp	Pro 30	His	Phe
Val	Val	Asp 35	Phe	Pro	Leu	Ser	Arg 40	Leu	Thr	Val	Cys	Phe 45	Asn	Ile	Asp
Gly	Gln 50	Pro	Gly	Asp	Ile	Leu 55	Arg	Leu	Val	Ser	Asp 60	His	Arg	Asp	Ser
Gly 65	Val	Thr	Val	Asn	Gly 70	Glu	Leu	Ile	Gly	Ala 75	Pro	Ala	Pro	Pro	Asn 80
Gly	His	Lys	Lys	Gln 85	Arg	Thr	Tyr	Leu	Arg 90	Thr	Ile	Thr	Ile	Leu 95	Ile
Asn	Lys	Pro	Glu 100	Arg	Ser	Tyr	Leu	Glu 105	Ile	Thr	Pro	Ser	Arg 110	Val	Ile
Leu	Asp	Gly 115	Gly	Asp	Arg	Leu	Val 120	Leu	Pro	Cys	Asn	Gln 125	Ser	Val	Val
Val	Gly 130	Ser	Trp	Gly	Leu	Glu 135	Val	Ser	Val	Ser	Ala 140	Asn	Ala	Asn	Val
Thr 145	Val	Thr	Ile	Gln	Gly 150	Ser	Ile	Ala	Phe	Val 155	Ile	Leu	Ile	His	Leu 160
Tyr	Lys	Lys	Pro	Ala 165	Pro	Phe	Gln	Arg	His 170	His	Leu	Gly	Phe	Tyr 175	Ile
Ala	Asn	Ser	Glu 180	Gly	Leu	Ser	Ser	Asn 185	Cys	His	Gly	Leu	Leu 190	Gly	Gln

0002260 " 69345569 " 092000

Phe	Leu	Asn 195	Gln	Asp	Ala	Arg	Leu 200	Thr	Glu	Asp	Pro	Ala 205	Gly	Pro	Ser
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Gln	Asn 210	Leu	Thr	His	Pro	Leu 215	Leu	Leu	Gln	Val	Gly 220	Glu	Gly	Pro	Glu
-----	------------	-----	-----	-----	-----	------------	-----	-----	-----	-----	------------	-----	-----	-----	-----

Ala 225	Val	Leu	Thr	Val	Lys 230	Gly	His	Gln	Val	Pro 235	Val	Val	Trp	Lys	Gln 240
------------	-----	-----	-----	-----	------------	-----	-----	-----	-----	------------	-----	-----	-----	-----	------------

Arg	Lys	Ile	Tyr	Asn 245	Gly	Glu	Glu	Gln	Ile 250	Asp	Cys	Trp	Phe	Ala 255	Arg
-----	-----	-----	-----	------------	-----	-----	-----	-----	------------	-----	-----	-----	-----	------------	-----

Asn	Asn	Ala	Ala 260	Lys	Leu	Ile	Asp	Gly 265	Glu	Tyr	Lys	Asp	Tyr 270	Leu	Ala
-----	-----	-----	------------	-----	-----	-----	-----	------------	-----	-----	-----	-----	------------	-----	-----

Ser	His	Pro 275	Phe	Asp	Thr	Gly	Met 280	Thr	Leu	Gly	Gln	Gly 285	Met	Ser	Arg
-----	-----	------------	-----	-----	-----	-----	------------	-----	-----	-----	-----	------------	-----	-----	-----

Glu	Leu 290
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<210> 193
<211> 87
<212> PRT
<213> homo sapiens

<400> 193

Gly 1	His	Gly	Ser	Tyr 5	Arg	Thr	Pro	Lys	Arg 10	Ser	Ser	Thr	Asn	Cys 15	Leu
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Gly	Lys	Phe	Trp 20	Glu	Leu	Ala	Asp	Ala 25	Lys	Lys	Lys	Arg	Lys 30	Lys	Val
-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----

His	Gln	Lys 35	Gln	Lys	Arg	Ala	Thr 40	Ile	Arg	Ala	Thr	Glu 45	Leu	Ala	Lys
-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----

Gly	Lys 50	Arg	His	Val	Gly	Gly 55	Ser	Val	Ser	His	Leu 60	Ser	Pro	Gly	Thr
-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----

Val 65	Lys	Cys	Val	Ile	Thr 70	Ala	Gln	Val	His	Gly 75	Lys	Arg	Gln	Gln	Gln 80
-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------

Lys	Ala	Leu	Cys	Arg 85	Leu	Glu
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<210> 194
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<212> PRT
<213> homo sapiens

<400> 194

Gln 1	Phe	Ile	Gln	Gly 5	Met	Cys	Ser	Arg	Lys 10	Phe	Ala	Trp	Tyr	Leu 15	Phe
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000260" 69594960

Ile Phe

<400> 195

Asp 1	Asp	Arg	Ser	His 5	Ala	Phe	His	His	His 10	Lys	Ser	Val	Ile	Asp 15	Ala
Met	Lys	Gly	Arg 20	Pro	Gly	Gln	Ser	Pro 25	Leu	Phe	Arg	Pro	Ser 30	Gln	Gly
Thr	Gly	Arg 35	Val	Pro	Gly	Thr	Arg 40	Gln	Met	Leu	Gln	Asp 45	Ser	Val	Gln
Ala	Ala 50	Leu	Glu	Glu	Val	Ala 55	Ala	Ser	Glu	Ala	Leu 60	Leu	Gly	Pro	Leu
Ser 65	Pro	Pro	Gly	Lys	Ser 70	Arg	Asp	Gly	Asn	Ala 75	Ser	Ala	Gly	Glu	Gly 80
Cys	Gln	Val	Phe	Arg 85	Ser	Pro	Pro	Ser	Glu 90	Val	Pro	Ser	Pro	Pro 95	Gly
Gln	Asp	Thr	Pro 100	Thr	Ser	Thr	Phe	Leu 105	Lys	Arg	Arg	Trp	Asp 110	Ser	Gln
Val	Thr	Leu 115	Leu	Pro	Ser	Lys	Lys 120	Cys	Lys	Ser	Gln	Gln 125	Leu	Gln	Glu
Ser	Val 130	Ser	Gln	Phe	Pro	Pro 135	Ser	Pro	Gly	Gly	Arg 140	Arg	Glu	Gly	Pro
Trp 145	Ser	Ser	Leu	Gly	Ala 150	Gly	Gly	Pro	Ser	Ser 155	His	Ile	Ser	Ala	Lys 160

Table 1. Demographic characteristics of the study population	
Age (years)	
18-24	10.0
25-34	15.0
35-44	20.0
45-54	25.0
55-64	30.0
65-74	35.0
75-84	40.0
85-94	45.0
95-104	50.0
105-114	55.0
115-124	60.0
125-134	65.0
135-144	70.0
145-154	75.0
155-164	80.0
165-174	85.0
175-184	90.0
185-194	95.0
195-204	100.0
205-214	105.0
215-224	110.0
225-234	115.0
235-244	120.0
245-254	125.0
255-264	130.0
265-274	135.0
275-284	140.0
285-294	145.0
295-304	150.0
305-314	155.0
315-324	160.0
325-334	165.0
335-344	170.0
345-354	175.0
355-364	180.0
365-374	185.0
375-384	190.0
385-394	195.0
395-404	200.0
405-414	205.0
415-424	210.0
425-434	215.0
435-444	220.0
445-454	225.0
455-464	230.0
465-474	235.0
475-484	240.0
485-494	245.0
495-504	250.0
505-514	255.0
515-524	260.0
525-534	265.0
535-544	270.0
545-554	275.0
555-564	280.0
565-574	285.0
575-584	290.0
585-594	295.0
595-604	300.0
605-614	305.0
615-624	310.0
625-634	315.0
635-644	320.0
645-654	325.0
655-664	330.0
665-674	335.0
675-684	340.0
685-694	345.0
695-704	350.0
705-714	355.0
715-724	360.0
725-734	365.0
735-744	370.0
745-754	375.0
755-764	380.0
765-774	385.0
775-784	390.0
785-794	395.0
795-804	400.0
805-814	405.0
815-824	410.0
825-834	415.0
835-844	420.0
845-854	425.0
855-864	430.0
865-874	435.0
875-884	440.0
885-894	445.0
895-904	450.0
905-914	455.0
915-924	460.0
925-934	465.0
935-944	470.0
945-954	475.0
955-964	480.0
965-974	485.0
975-984	490.0
985-994	495.0
995-1004	500.0
1005-1014	505.0
1015-1024	510.0
1025-1034	515.0
1035-1044	520.0
1045-1054	525.0
1055-1064	530.0
1065-1074	535.0
1075-1084	540.0
1085-1094	545.0
1095-1104	550.0
1105-1114	555.0
1115-1124	560.0
1125-1134	565.0
1135-1144	570.0
1145-1154	575.0
1155-1164	580.0
1165-1174	585.0
1175-1184	590.0
1185-1194	595.0
1195-1204	600.0
1205-1214	605.0
1215-1224	610.0
1225-1234	615.0
1235-1244	620.0
1245-1254	625.0
1255-1264	630.0
1265-1274	635.0
1275-1284	640.0
1285-1294	645.0
1295-1304	650.0

Ser 1	His	Thr	Met	His 5	Cys	Lys	Glu	Thr	Lys 10	Gln	Leu	Tyr	Arg	Ser 15	Gly
Asp	Ala	Ser	Val 20	Tyr	Asn	Thr	Phe	Met 25	Ser	Arg	Ile	Arg	Ser 30	Arg	His
Gln	Asp	Leu 35	Tyr	Thr	Val	Ala	Ala 40	Ala	Ile	Gly	Thr	Met 45	Ile	Gln	Asn
Ile	Lys 50	Tyr	Ile	Ser	Ile	Tyr 55	Ile	Asn	Thr	Gln	Leu 60	Gly	Trp	Gly	Arg

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Met 65	Leu	Gly	Asp	Leu	Val 70	Ser	Pro	Ala	Glu	Gly 75	Leu	Gly	Gly	Arg	Glu 80
Gly	Gly	Gly	Lys	Gly 85	Phe	Leu	Thr	Phe	Val 90	Leu	Asn	Asp	Gly	Ser 95	Glu
Gly	Arg	Arg	Glu 100	Met	Gly	Lys	His	Ser 105	Leu	His	Thr	Leu	Met 110	Cys	Ser
His	Thr	His 115	Ala	Gln	Thr	Lys	His 120	Arg	His	Arg	Arg	Val 125	Ser	Asn	Ser
Leu	Thr 130	Leu	Ile	Gly	Lys	Gln 135	Ala	Trp	Asp	Ile	Pro 140	Leu	Gln		

<210> 199
 <211> 189
 <212> PRT
 <213> homo sapiens

<400> 199

Gln 1	Cys	Arg	Gly	Phe 5	Asn	Leu	Lys	Ala	Tyr 10	Arg	Asn	Ala	Ala	Glu 15	Ile
Val	Gln	Tyr	Gly 20	Val	Lys	Asn	Asn	Thr 25	Thr	Phe	Leu	Glu	Cys 30	Ala	Pro
Lys	Ser	Pro 35	Gln	Ala	Ser	Ile	Lys 40	Trp	Leu	Leu	Gln	Lys 45	Asp	Lys	Asp
Arg	Arg 50	Lys	Glu	Val	Lys	Leu 55	Asn	Glu	Arg	Ile	Ile 60	Ala	Thr	Ser	Gln
Gly 65	Leu	Leu	Ile	Arg	Ser 70	Val	Gln	Gly	Ser	Asp 75	Gln	Gly	Leu	Tyr	His 80
Cys	Ile	Ala	Thr	Glu 85	Asn	Ser	Phe	Lys	Gln 90	Thr	Ile	Ala	Lys	Ile 95	Asn
Phe	Lys	Val	Leu 100	Asp	Ser	Glu	Met	Val 105	Ala	Val	Val	Thr	Asp 110	Lys	Trp
Ser	Pro	Trp 115	Thr	Trp	Ala	Ser	Ser 120	Val	Arg	Ala	Leu	Pro 125	Phe	His	Pro
Lys	Asp 130	Ile	Met	Gly	Ala	Phe 135	Ser	His	Ser	Glu	Met 140	Gln	Met	Ile	Asn
Gln 145	Tyr	Cys	Lys	Asp	Thr 150	Arg	Gln	Gln	His	Gln 155	Gln	Gly	Asp	Glu	Ser 160

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112

Gln Lys Met Arg Gly Asp Tyr Gly Lys Leu Lys Ala Leu Ile Asn Ser
165 170 175

Arg Lys Ser Arg Asn Arg Arg Asn Gln Leu Pro Glu Ser
180 185

<210> 200

<211> 97

<212> PRT

<213> homo sapiens

<400> 200

Phe Phe Arg Glu Ala Glu Ser Pro Phe Val Ala Arg Leu Glu Cys Ser
1 5 10 15

Gly Ala Ile Ser Ala His Cys Ser Thr Val Ser Ala His Cys Ser Leu
20 25 30

Arg Pro Pro Val Phe Lys Arg Phe Ser Cys Leu Ser Leu Leu Ser Ser
35 40 45

Trp Asp Tyr Arg Cys Ala Pro Pro Arg Pro Ala Asn Phe Cys Ile Phe
50 55 60

Ser Arg Asp Gly Val Ser Leu Cys Trp Pro Gly Trp Ser Gln Ser Arg
65 70 75 80

Pro Arg Asp Pro Ala His Leu Gly Leu Pro Lys Cys Trp Asp Tyr Arg
85 90 95

Xxx

<210> 201

<211> 250

<212> PRT

<213> homo sapiens

<400> 201

Glu Thr Arg Val Lys Thr Ser Leu Glu Leu Leu Arg Thr Gln Leu Glu
1 5 10 15

Pro Thr Gly Thr Val Gly Asn Thr Ile Met Thr Ser Gln Pro Val Pro
20 25 30

Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
35 40 45

Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
50 55 60

His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
65 70 75 80

000260" 9994960

000060-000000

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<210> 202
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<212> PRT
<213> homo sapiens
<400> 202
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Glu 1	Lys	Thr	Pro	Gly 5	Phe	Glu	Trp	Lys	Leu 10	Thr	Ala	Glu	Ser	His 15	Arg
Pro	Arg	Gln	Gln 20	Gln	Arg	Gln	Gln	Gln 25	Thr	Phe	Gly	Ile	Leu 30	Phe	Ser
Thr	His	Val 35	Leu	Ile	Ile	His	Leu 40	Ile	Ile	Phe	Leu	Val 45	Glu	Lys	Leu
Gln	Ile 50	Ser	Leu	Phe	Asn	Ile 55	Tyr	Ile	Gln	Phe	Asn 60	Lys	Pro	Leu	Ala

114

Ser Tyr Leu Phe Ser His Leu Arg Tyr Phe Phe Pro Pro His Leu Ala
65 70 75 80

Pro Val Pro Pro Phe Leu Phe Ser Leu Cys Lys Arg Lys Tyr Leu Thr
85 90 95

Tyr Leu Gly Pro Thr Ser Ile Met
100

<210> 203

<211> 93

<212> PRT

<213> homo sapiens

<400> 203

His Lys Lys Asn Phe Trp Gln Ile Phe Ile Gln Ile Ala Cys Leu Gln
1 5 10 15

Trp Gln Ile Ser Gln His Phe Ser Leu Phe Cys Leu Cys Leu Ser Leu
20 25 30

Cys Ile Phe Leu Glu Arg Lys Leu Asn Ala Phe Asn Val Leu Ile Ile
35 40 45

Thr Leu Leu Lys Leu Asp Pro Asn Met Leu Asn Ile Ser Ser Cys Lys
50 55 60

Gly Arg Arg Gly Arg Glu Glu Gln Gly Gln Gly Glu Glu Lys Asn
65 70 75 80

Thr Ser Gly Glu Arg Thr Ser Asn Leu Gln Glu Ala Tyr
85 90

<210> 204

<211> 113

<212> PRT

<213> homo sapiens

<400> 204

Arg Pro Lys Pro Gly His Pro Leu Tyr Ser Lys Tyr Met Arg Gly Asp
1 5 10 15

Val Leu Val Met Leu Lys Gln Thr Glu Asn Asn Tyr Leu Glu Cys Gln
20 25 30

Lys Gly Glu Asp Thr Gly Arg Val His Leu Ser Gln Met Lys Ile Ile
35 40 45

Thr Pro Leu Asp Glu His Leu Arg Ser Arg Pro Asn Asp Pro Ser His
50 55 60

Ala Gln Lys Pro Val Asp Ser Gly Ala Pro His Ala Val Val Leu His
65 70 75 80

000260"6954960



Ile Gly Leu Ser Ser Gly Glu Asp Arg Tyr Arg Leu Val Gln Arg Glu
100 105 110

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<210> 205
<211> 225
<212> PRT
<213> homo sapiens
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Thr Ser Leu Leu Glu Lys Leu Val Tyr Leu Leu Glu Lys Ile Asp Thr
1 5 10 15

Asn Tyr Val Lys Val Ile Ile Asp Ile Pro Glu Gly Gly Asn Gly Lys
35 40 45

Arg Glu Cys Val Ser Ser His Cys Val Lys Gly Ser Arg Cys Val Ala
50 55 60

Arg Phe Glu Tyr Ile Gly Glu Gln Lys Asp Glu Leu Ser Phe Ser Glu
65 70 75 80

Gly Glu Ile Ile Ile Leu Lys Glu Tyr Val Asn Glu Glu Trp Ala Arg
85 90 95

Gly Glu Val Arg Gly Arg Thr Gly Ile Phe Pro Leu Asn Phe Val Glu
100 105 110

Pro Val Glu Asp Tyr Pro Thr Ser Gly Ala Asn Val Leu Ser Thr Lys
115 120 125

Val	Pro	Leu	Lys	Thr	Lys	Lys	Glu	Asp	Ser	Gly	Ser	Asn	Ser	Gln	Val
	130					135					140				

Asn	Ser	Leu	Pro	Ala	Glu	Trp	Cys	Glu	Ala	Leu	His	Ser	Phe	Thr	Ala
145					150					155					160

Glu Thr Ser Asp Asp Leu Ser Phe Lys Arg Gly Asp Arg Ile Gln Ile
165 170 175

Leu Glu Arg Leu Asp Ser Asp Trp Cys Arg Gly Arg Leu Gln Asp Arg
180 185 190

116

Glu Gly Ile Phe Pro Ala Val Phe Val Arg Pro Cys Pro Ala Glu Ala
195 200 205

Lys Ser Met Leu Ala Ile Val Pro Lys Gly Gln Glu Gly Gln Ser Leu
210 215 220

Ile
225

<210> 206
<211> 105
<212> PRT
<213> homo sapiens

<400> 206

Cys Ile Gly Phe Ser Ser Gly Phe Asp Lys Val Lys Arg Ile Val Thr
1 5 10 15

Arg Val Thr Gln Thr Cys Gln Leu Ser Glu Ser Leu Val Val Lys Pro
20 25 30

Glu Leu Gly Lys Leu Ser Leu Arg Arg Leu Lys Glu Arg Ala Gln Val
35 40 45

Gly Ile Cys Val Ile Thr Val Leu Leu Pro Arg His Gly Val Asp Asn
50 55 60

Lys Ile Pro Leu Gln Ser Thr Gly Val Ser Val Arg Leu Val Leu Gln
65 70 75 80

Lys Ala Ala His Trp Glu Trp Gly Gly Ala Cys Gly Lys Pro Asp Cys
85 90 95

Gly Glu Lys Leu Gly Glu Asn Gly Ser
100 105

<210> 207
<211> 83
<212> PRT
<213> homo sapiens

<400> 207

Leu Cys Gly Ala Ala Ala Ser Cys Met Met Leu Gly Ser Leu Ala Pro
1 5 10 15

Asp Pro Gly Ser Arg Arg His Ser Gly Gln Ala Ala Leu Arg Pro Arg
20 25 30

Arg Tyr Pro Thr Leu Trp Asp Arg Cys Arg Lys Arg Trp Leu Arg Pro
35 40 45

Ile Phe Thr Gln Leu Leu Ala Ala Val Trp Leu Thr Thr Arg Ser Ser
50 55 60

000260"69594960



Pro Phe Pro Val Ser Arg Phe Leu Gln His Gln Ala Asn Thr Tyr Thr
65 70 75 80

Ser Ala Leu

<210> 208

<211> 581

<212> PRT

<213> homo sapiens

<400> 208

Tyr 1	Phe	Cys	Met	Met 5	Thr	Glu	Ala	Glu	Gln 10	Asp	Lys	Trp	Gln	Ala 15	Val
Leu	Gln	Asp	Cys 20	Ile	Arg	His	Cys	Asn 25	Asn	Gly	Ile	Pro	Glu 30	Asp	Ser
Lys	Val	Glu 35	Gly	Pro	Ala	Phe	Thr 40	Asp	Ala	Ile	Arg	Met 45	Tyr	Arg	Gln
Ser	Lys 50	Glu	Leu	Tyr	Gly	Thr 55	Trp	Glu	Met	Leu	Cys 60	Gly	Asn	Glu	Val
Gln 65	Ile	Leu	Ser	Asn	Leu 70	Val	Met	Glu	Glu	Leu 75	Gly	Pro	Glu	Leu	Lys 80
Ala	Glu	Leu	Gly	Pro 85	Arg	Leu	Lys	Gly	Lys 90	Pro	Gln	Glu	Arg	Gln 95	Arg
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Ala	Lys	Ala 115	Arg	Phe	Glu	Glu	Val 120	Leu	Ser	Lys	Val	Gln 125	Gln	Val	Gln
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Ala	Glu	Val	Cys	Val 165	Arg	Asn	His	Val	Gln 170	Pro	Tyr	Ile	Pro	Ser 175	Ile
Leu	Glu	Ala	Leu 180	Met	Val	Pro	Thr	Ser 185	Gln	Gly	Phe	Thr	Glu 190	Val	Arg
Asp	Val	Phe 195	Phe	Lys	Glu	Val	Thr 200	Asp	Met	Asn	Leu	Asn 205	Val	Ile	Asn

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Glu	Gly 210	Gly	Ile	Asp	Lys	Leu 215	Gly	Glu	Tyr	Met	Glu 220	Lys	Leu	Ser	Arg
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Ser	Leu	Arg	Leu	Asp 245	Gly	Leu	Gln	Gln	Arg 250	Phe	Asp	Val	Ser	Ser 255	Thr
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Arg 305	Val	Leu	Lys	Lys	Tyr 310	Asp	Tyr	Asp	Ser	Ser 315	Ser	Val	Arg	Lys	Arg 320
Phe	Phe	Arg	Glu	Ala 325	Leu	Leu	Gln	Ile	Ser 330	Ile	Pro	Phe	Leu	Leu 335	Lys
Lys	Leu	Ala	Pro 340	Thr	Cys	Lys	Ser	Glu 345	Leu	Pro	Arg	Phe	Gln 350	Glu	Leu
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Glu 385	Ala	Ala	Val	Gln	Arg 390	Lys	His	Asn	Leu	Tyr 395	Arg	Asp	Ser	Met	Val 400
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Ala	Pro	Ala 435	Pro	Arg	Ser	Gln	Pro 440	Pro	Ser	Arg	Lys	Ser 445	Asp	Gly	Ala
Pro	Ser 450	Arg	Trp	Ser	Leu	Trp 455	Ser	Arg	Met	Arg	Arg 460	Trp	Gly	Cys	Pro

Leu 465	Arg	Leu	Ala	Leu	Ser 470	His	His ¹¹⁹	His	Leu	Arg 475	Pro	Arg	Thr	Val	Ser 480
Leu	Arg	Ser	Glu	Ala 485	Cys	Trp	Pro	Lys	Val 490	Cys	Gly	Leu	Arg	Ala 495	Pro
His	Gln	Pro	Ala 500	Pro	Cys	Ser	Thr	Gly 505	Pro	Pro	Leu	Gly	Arg 510	Val	Pro
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Trp	Gly	Trp 35	Ala	Ala	Ala	Pro	Ala 40	Ala	Val	Ala	Val	Leu 45	Leu	Ala	Pro
Val	Asp 50	Gly	Gly	Ala	Leu	Gly 55	Gln	Gln	Val	Gln	Val 60	Gly	Val	Ala	Val
Val 65	His	Asp	His	Ala	Val 70	Pro	Val	Glu	Val	Val 75	Leu	Pro	Leu	His	Arg 80
Gly	Leu	Leu	His	Ser 85	Leu	Gln	Asp	Val	Leu 90	His	Asp	Gly	Leu	Gln 95	His
His	Leu	Leu	Val 100	Arg	Val	Phe	His	Gln 105	Asp	Glu	Pro	Gly	Lys 110	Val	Leu

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Systematic Gene Search in the Incyte LifeSeq Database

Normal tissue
~50,000 individual ESTs

Tumor tissue
~50,000 individual ESTs

Priority list
High

Prostate
Breast
Ovary
Bladder
Uterus

Iterative assembling
with
increasing mismatch

Low

~8,000 contigs
+
~25,000 individual sequences

~8,000 contigs
+
~25,000 individual sequences

Comparison of databases

normal tissue-
specific
(expected: 100-500)

nonspecifically
expressed genes

tumor tissue-
specific
(expected: 100-500)

Genes of Interest

Figure 1

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Systematische Gen-Suche in der Incyte LifeSeq Datenbank

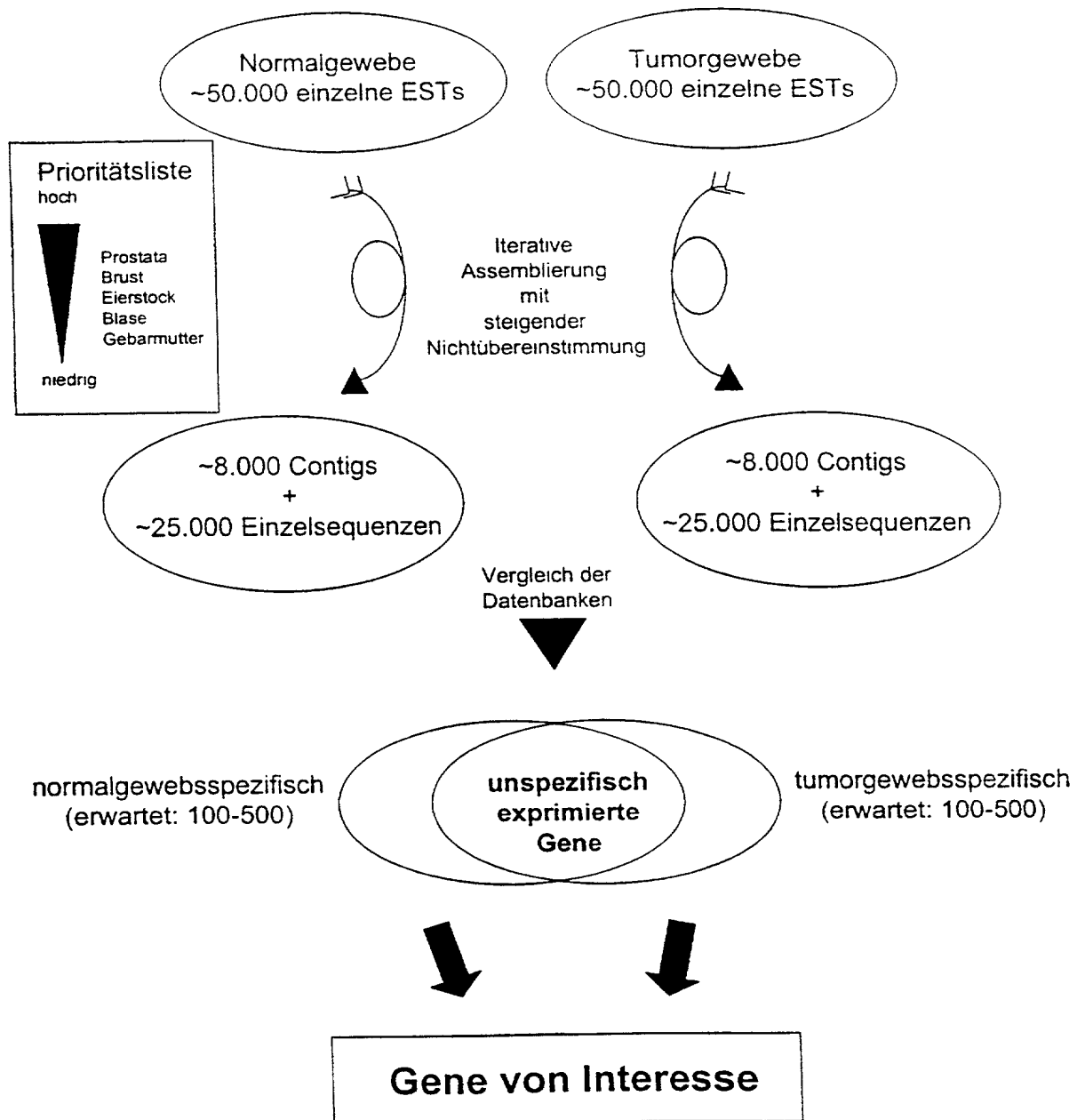


Fig. 1

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Principle of EST Assembly

~50,000 ESTs per tissue

Assembly at 0% mismatch
with GAP4 (Staden)

Contigs

Individual Sequences

Contigs increasing in
number and lengthIterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000-6000 contigs

~25,000 other
individual sequences~30,000 consensus-
sequences per tissue

Figure 2a

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Prinzip der EST-Assemblierung

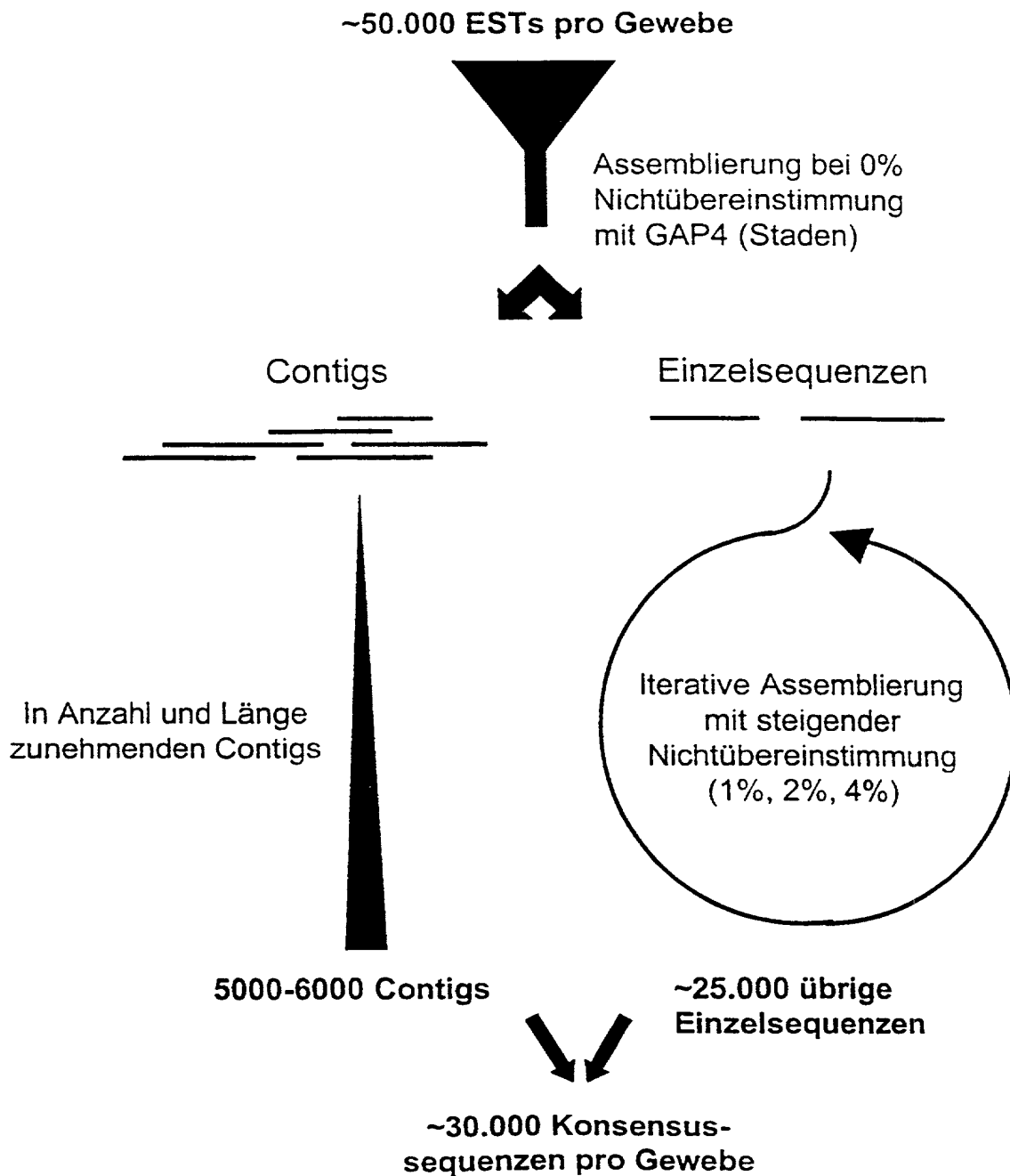


Fig. 2a

~50,000 ESTs of a tissue (e.g.: uterus tumor)

```
GAP4 Assembly 1st Round:
minimum initial match: 20
maximum number of inserted blanks per
sequence: 8
maximum percent mismatch: 0
```

GAP4 Database 1	unassembled
Contigs 1	ESTs
Individual sequences 1	

```
GAP4 Assembly 2nd Round:
minimum initial match: 20
maximum number of inserted blanks per
sequence: 8
maximum percent mismatch: 1
```

```
GAP4 Database 2                unassembled
Contigs 2                      ESTs
Individual sequences 2
```

GAP4 Assembly 3rd Round:
minimum initial match: 20
maximum number of inserted blanks per
sequence: 8
maximum percent mismatch: 2

```

GAP4 Database 3:      unassembled
Contigs 3             ESTs
Individual sequences 3

```

Figure 2b1

1990-1991		1991-1992		1992-1993		1993-1994		1994-1995		1995-1996		1996-1997		1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217	
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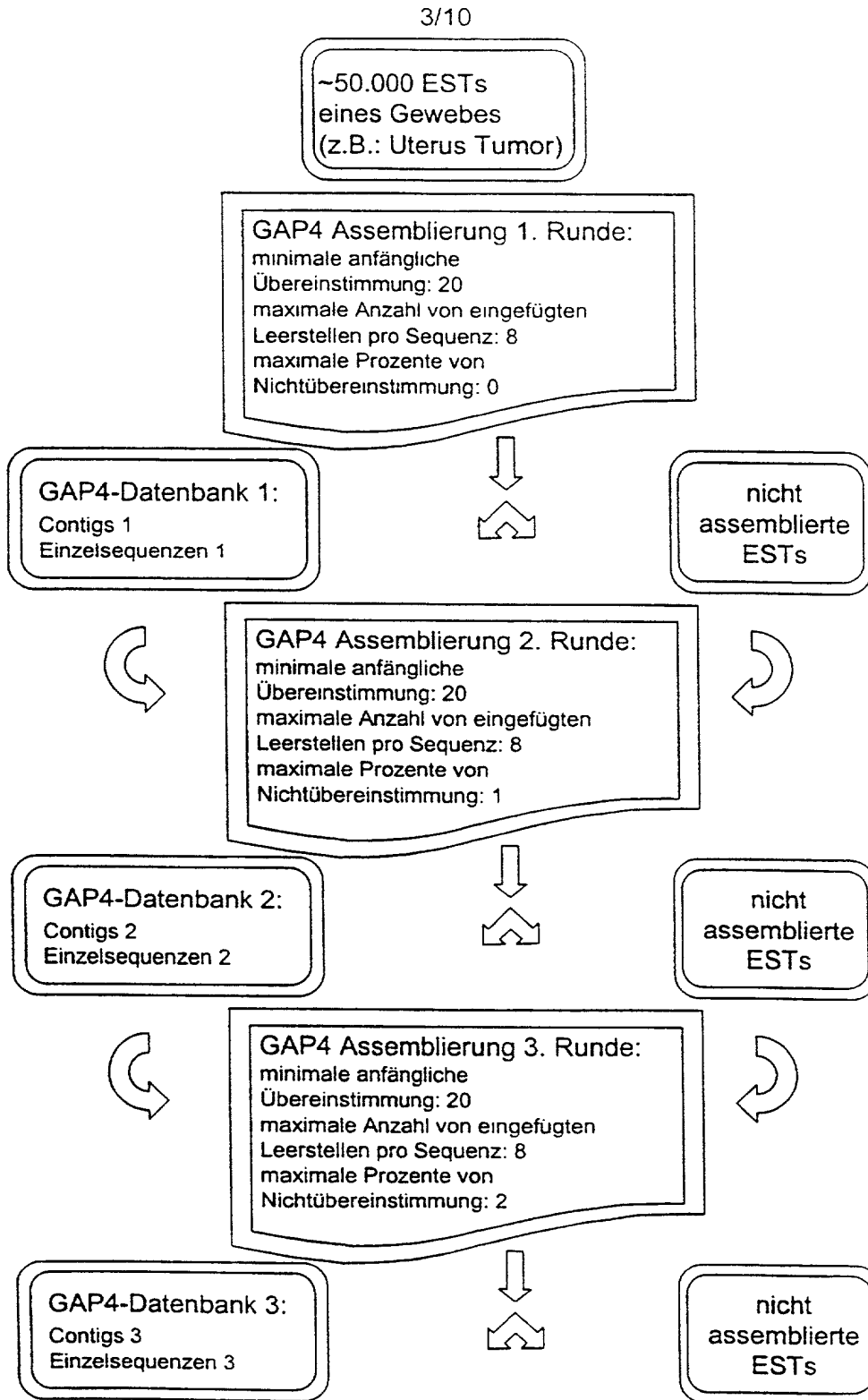


Fig. 2b1

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GAP4 Database 3:
Contigs 3
Individual seq. 3

unassembled
ESTs

Consensus 3

GAP4 Assembly 4th Round:
minimum initial match: 20
maximum number of inserted blanks per
sequence: 8
maximum percent mismatch: 2

GAP4 Database 4:
Contigs 4
Individual seq. 4

unassembled
ESTs

Consensus 4

GAP4 Assembly 5th Round:
minimum initial match: 20
maximum number of inserted blanks per
sequence: 8
maximum percent mismatch: 4

GAP4 Database 5:
Contigs 5
Individual seq. 5

unassembled
ESTs 5

Consensus 5

Individual Sequences 5

Figure 2b2

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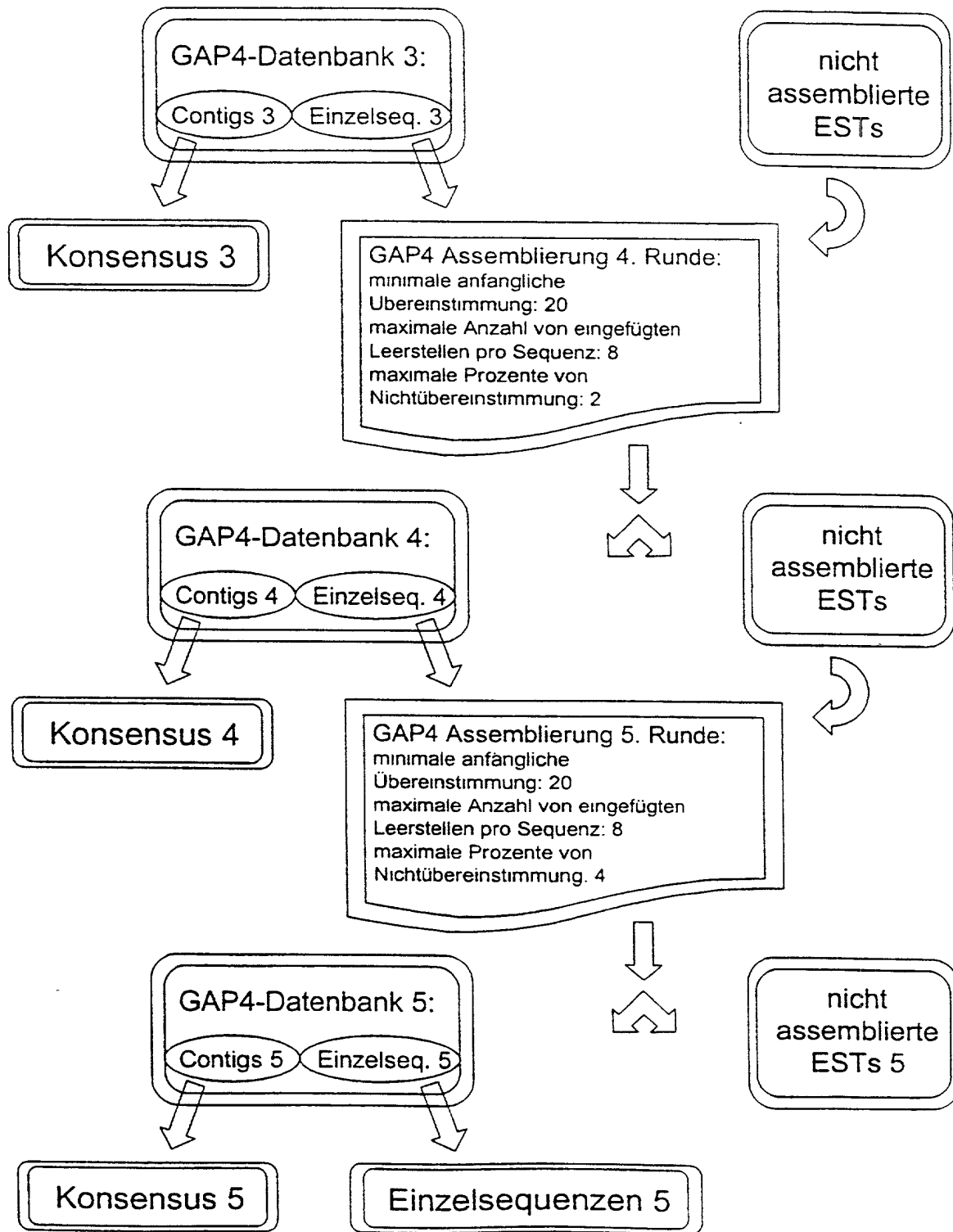


Fig. 2b2

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Consensus 3

Individual Sequences 5

Consensus 4

unassembled
ESTs 5

Consensus 5

GAP4 Assembly 6th Round:
minimum initial match: 20
maximum number of inserted blanks per
sequence: 8
maximum percent mismatch: 4

Assembled database
of a specific tissue
(e.g.: uterus tumor)

Figure 2b3

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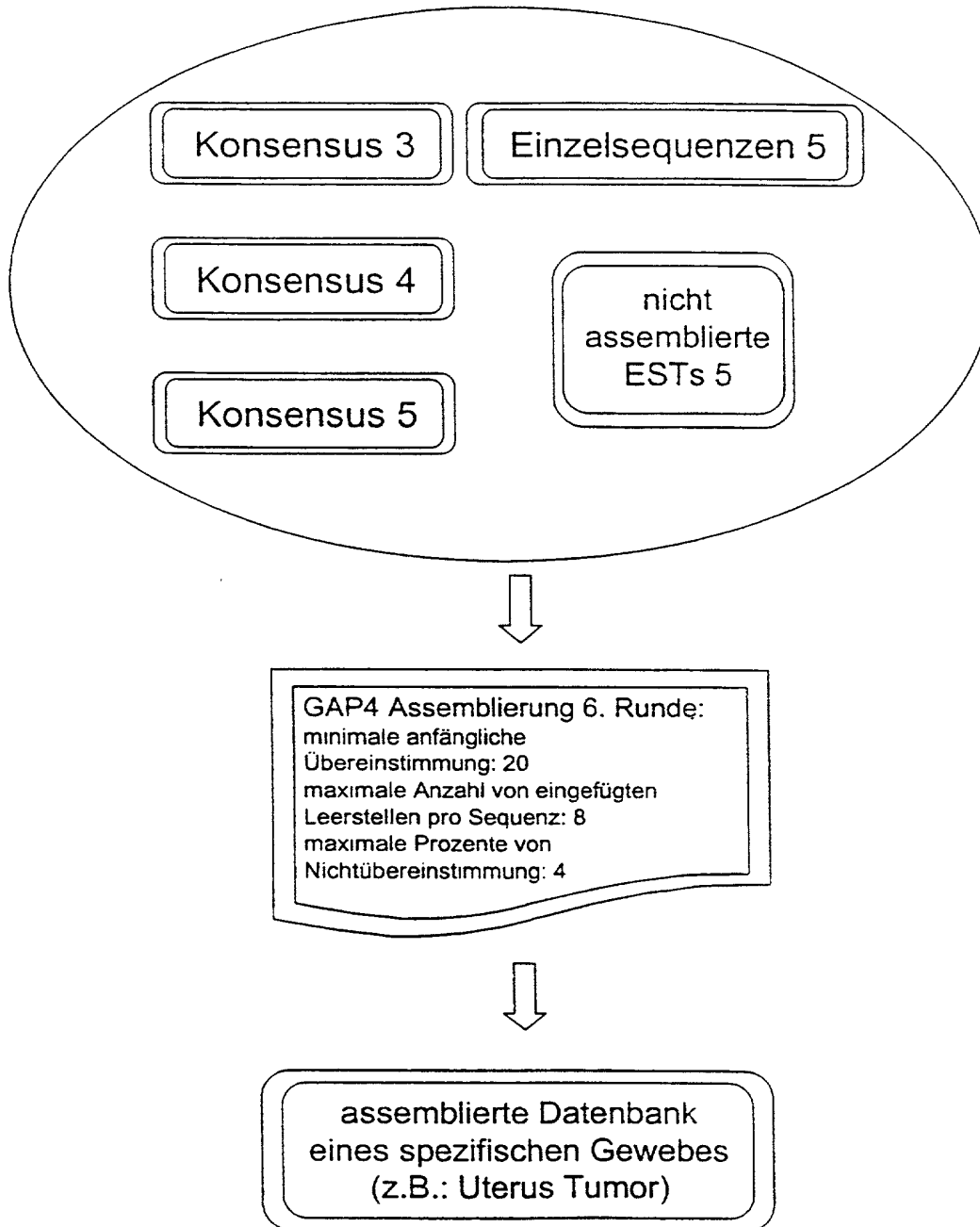


Fig. 2b3

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Assembled database
of a specific tissue
(e.g.: uterus tumor)

Consensus 6

Read-in as individual sequences

Database
of a specific tissue
(e.g.: uterus tumor)

Database of a second
specific tissue
(e.g.: normal uterus)

GAP4 Assembly
minimum initial match: 20
maximum number of inserted blanks per
sequence: 8
maximum percent mismatch: 4

Tumor tissue-
specific ESTs

Non-tissue-
specific ESTs

Normal tissue-
specific ESTs

Fig. 2b4

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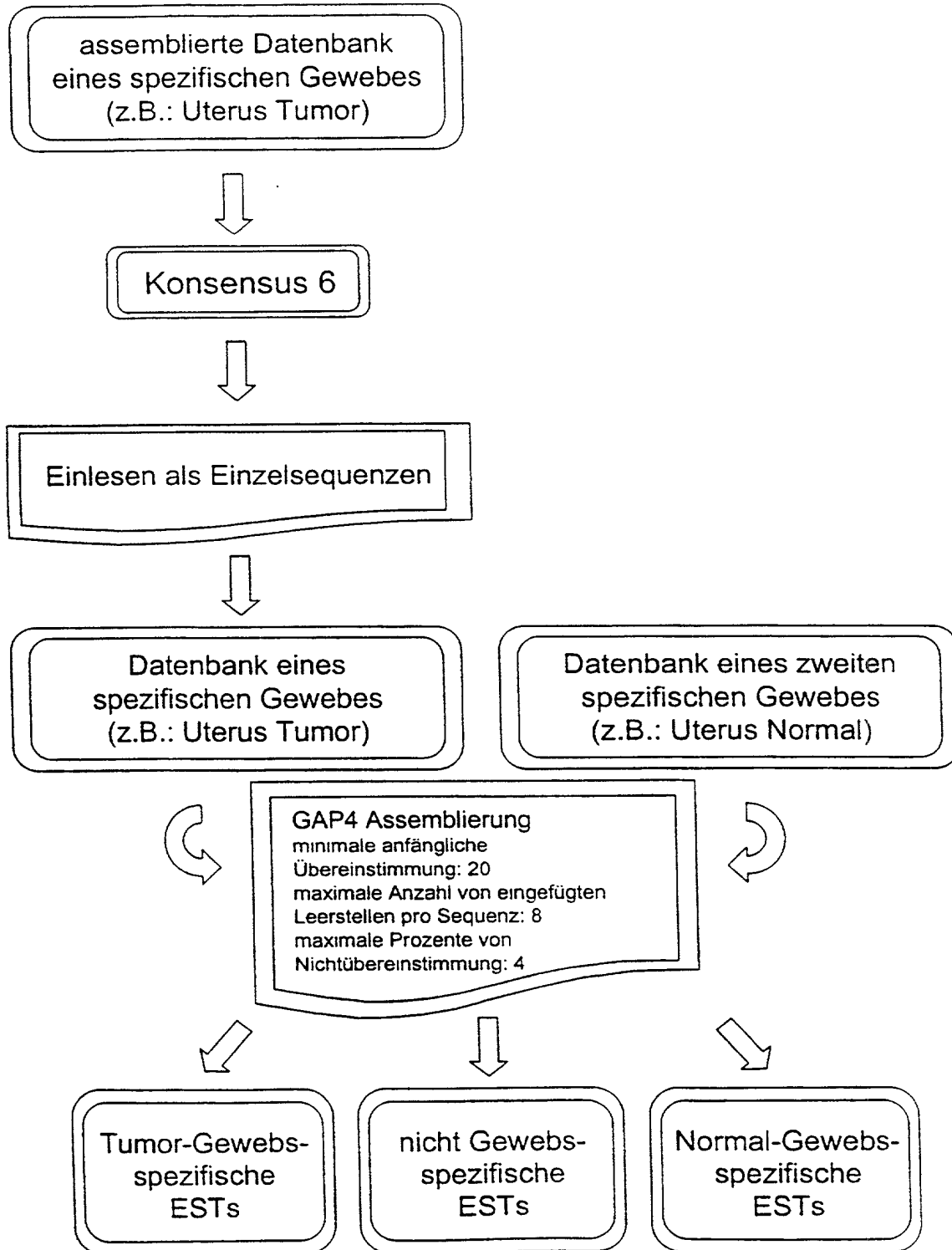


Fig. 2b4

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In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
tumor tissue

Assembly at 4% mismatch

Normal tissue
Specific genes

Cancer tissue
Specific genes

Genes expressed in both tissues

Figure 3

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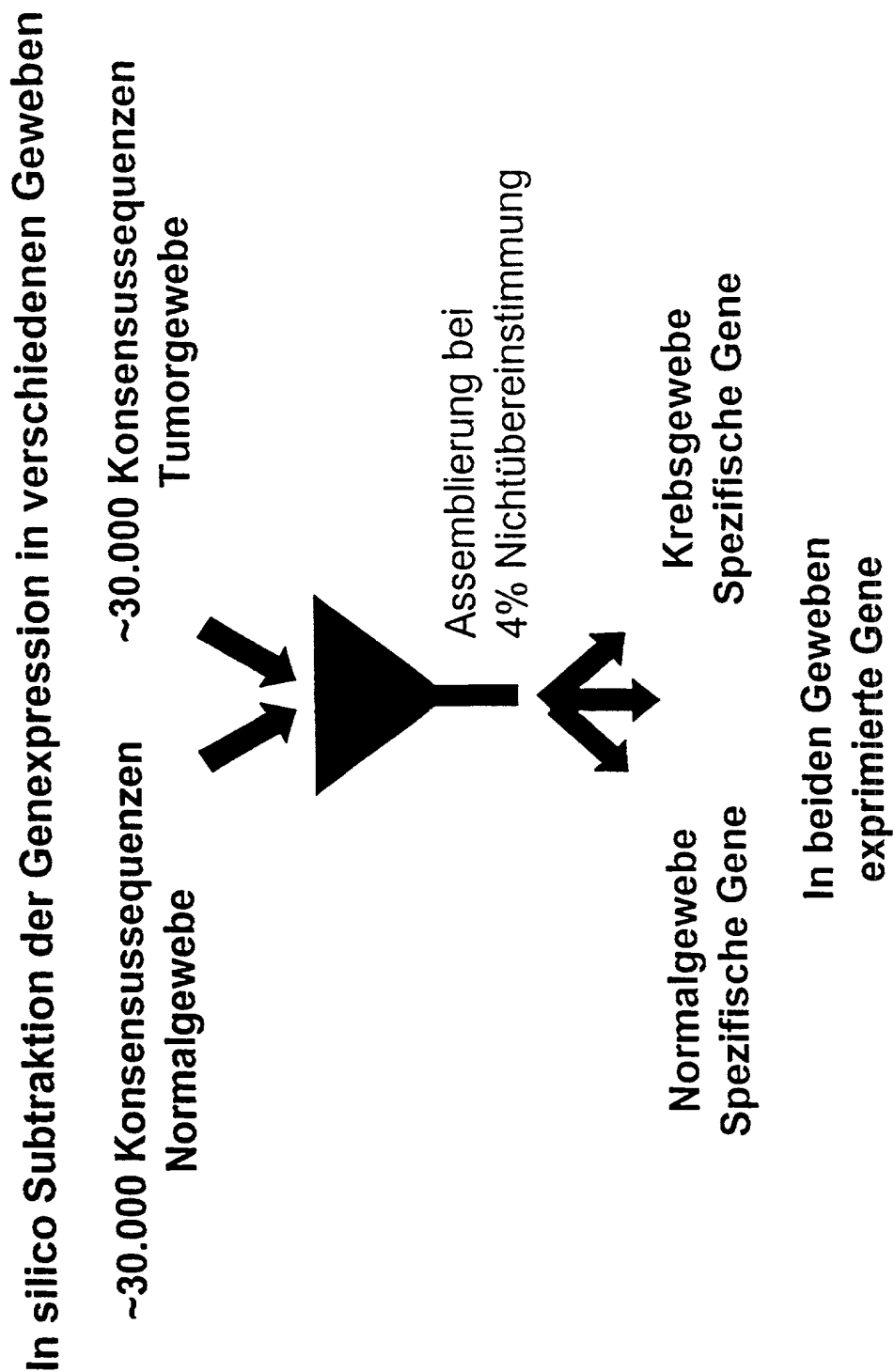


Fig. 3

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Genes of interest

Determination of tissue-specific expression
via electronic Northern (INCYTE LifeSeq and
public EST databases)

Candidate genes for tumor suppressors or
tumor activators

Figure 4a

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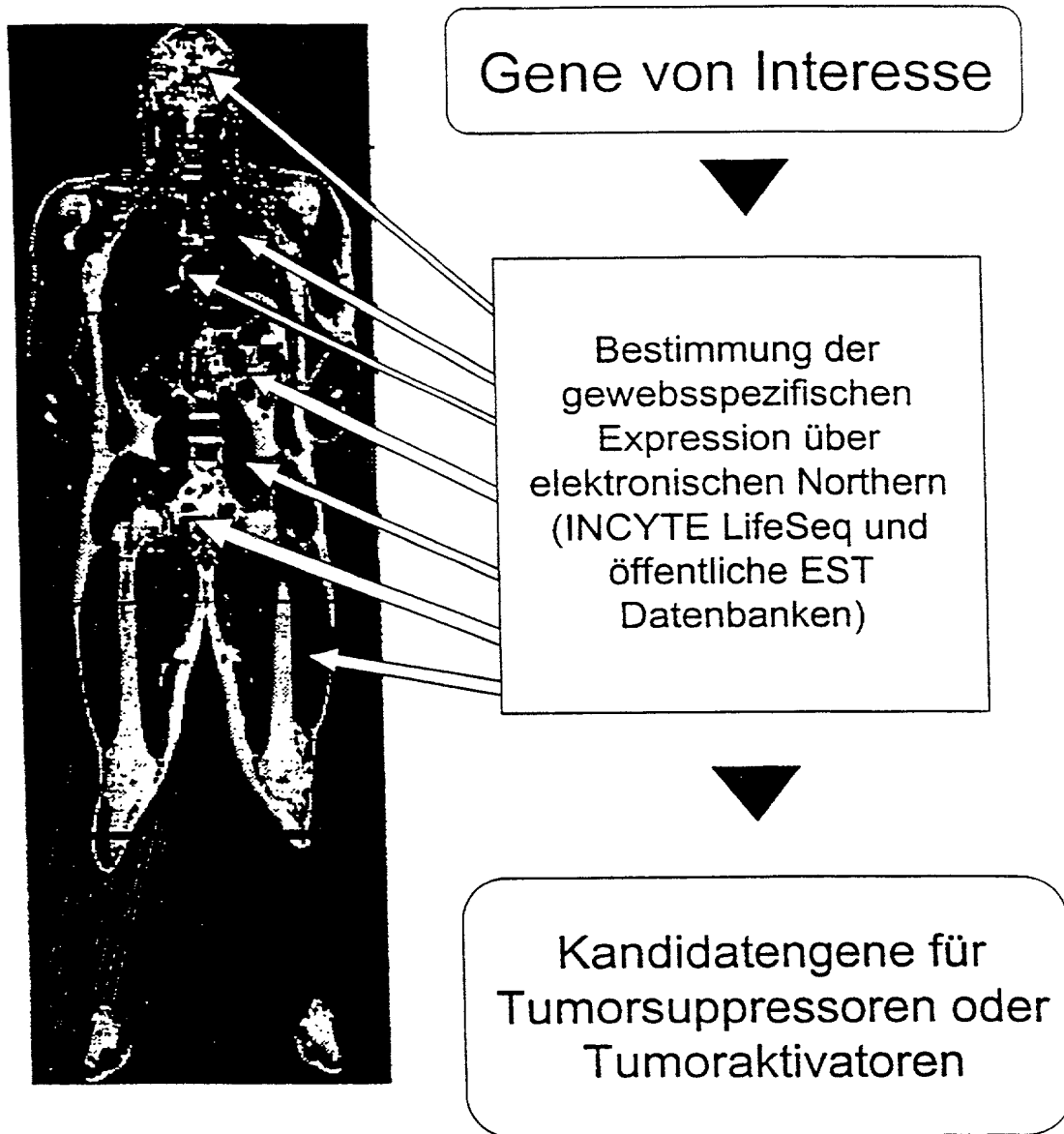


Fig. 4a

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Partial cDNA sequence
e.g., EST or contig
S

...GCCTCAAGTTATC...

WHILE $C_i > C_{i-1}$

Electronic Northern Blot

Fisher's Exact Test IF H_0 EXIT

Automatic Lengthening

Consensus sequence C

...ATGTCCTAGCCTCAAGTTATCAGATGCAA...

Figure 4b

REPLACEMENT PAGE (RULE 26)

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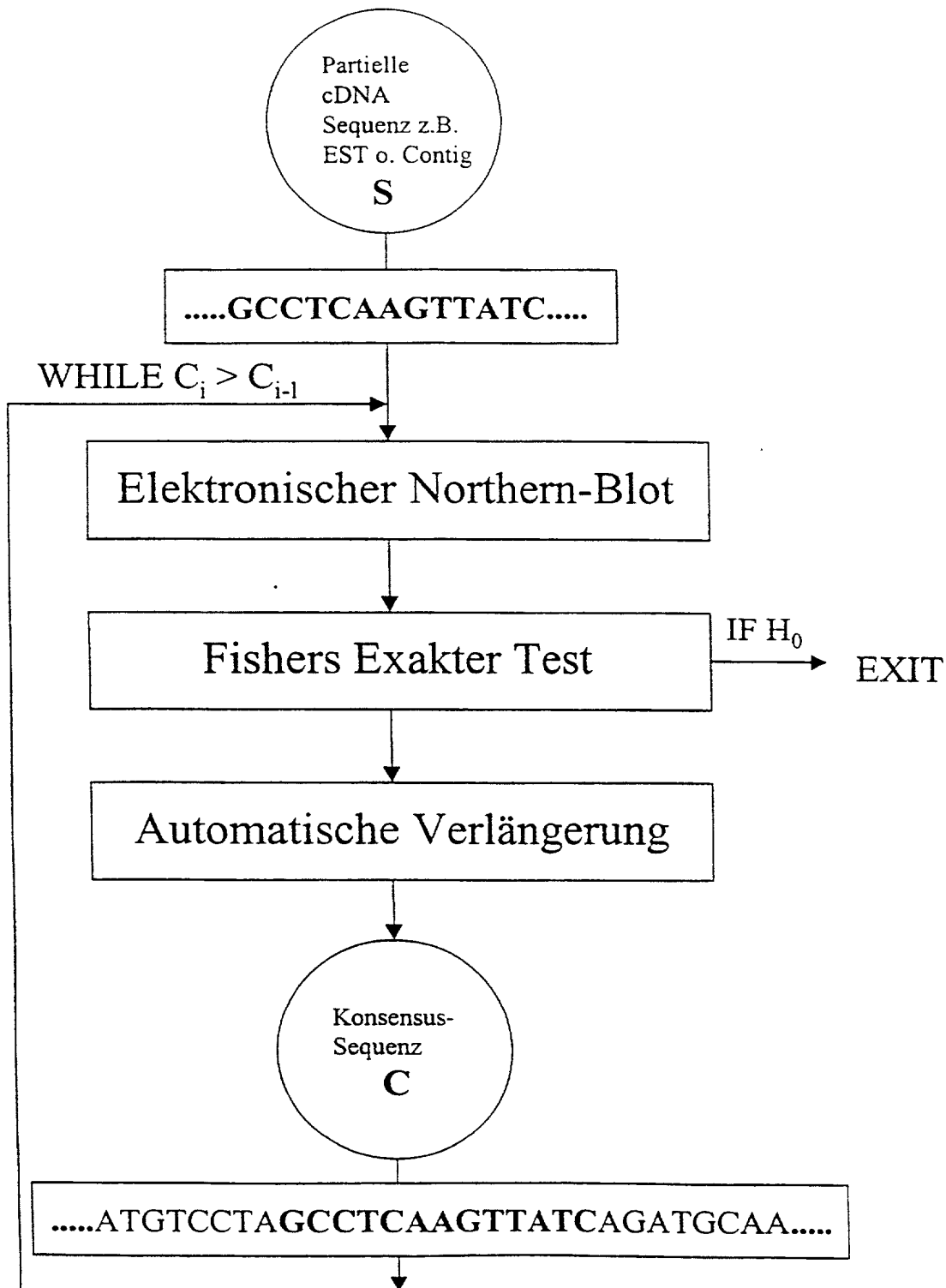


Fig. 4b

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Isolation of genomic BAC and PAC clones

Chromosomal clone localization via FISH

Hybridization signal

Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes

Exon Intron

Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

Figure 5

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Isolieren von genomischen BAC und PAC Klonen



Chromosomale Klon-Lokalisation über FISH



Hybridisierungssignal



Sequenzierung von Klonen, die in Regionen lokalisiert sind, die chromosomale Deletionen in Prostata- und Brustkrebs aufweisen, führt zur Identifizierung von Kandidatengenen



Bestätigung der Kandidatengene durch Screening von Mutationen und/oder Deletionen in Krebsgeweben

Fig. 5